

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:39:05 : Search time 48.75 Seconds
(without alignments)
26.467 Million cell updates/sec

Title: US-09-647-749A-1

Perfect score: 5

Sequence: 1 LESYT 5

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1349

Minimum DB seq length: 4

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	60.0	8	4	Q15898 homo sapien
2	2	40.0	8	2	Q9R3X0 planktothri
3	2	40.0	8	2	P72221 pseudomonas
4	2	40.0	8	4	Q9Y4J4 homo sapien
5	2	40.0	8	4	Q9Y4J3 homo sapien
6	2	40.0	8	4	O60773 homo sapien
7	2	40.0	8	5	Q94623 manduca sex
8	2	40.0	8	6	Q9XSY1 canis famil
9	2	40.0	8	8	Q8W8G2 diadema sav
10	2	40.0	8	8	Q8W8G4 diadema mex
11	2	40.0	8	8	Q8W8G6 diadema mex
12	2	40.0	8	8	Q8W8G5 diadema ant
13	2	40.0	8	8	Q8W8G3 diadema pau
14	2	40.0	8	8	Q34909 locusta mig
15	2	40.0	8	8	Q8WFR5 diadema pau
16	2	40.0	8	8	Q9XNP8 boophilus m

17	2	40.0	8	10	Q9SB24
18	2	40.0	8	11	Q9ET18
19	2	40.0	8	11	Q9ET17
20	2	40.0	8	11	Q9ET16
21	2	40.0	8	12	Q9WJ33
22	2	40.0	8	12	O83332
23	2	40.0	9	2	P72345
24	2	40.0	9	2	Q57328
25	2	40.0	9	2	Q44377
26	2	40.0	9	2	Q44468
27	2	40.0	9	2	Q43928
28	2	40.0	9	2	Q44001
29	2	40.0	9	4	Q96T78
30	2	40.0	9	4	Q9AVF9
31	2	40.0	9	4	Q15892
32	2	40.0	9	4	P78484
33	2	40.0	9	5	Q9TVF1
34	2	40.0	9	5	P82208
35	2	40.0	9	6	Q28093
36	2	40.0	9	8	O8WFT4
37	2	40.0	9	8	O8WFS4
38	2	40.0	9	8	O8W8X4
39	2	40.0	9	8	O8W8W5
40	2	40.0	9	8	O8W8W6
41	2	40.0	9	8	Q31653
42	2	40.0	9	10	P82440
43	2	40.0	9	11	Q9QWQ2
44	2	40.0	9	11	Q9QWT0
45	2	40.0	9	11	Q9QZ48

ALIGNMENTS

RESULT 1

Q15898 PRELIMINARY; PRT; 8 AA.
ID Q15898
AC Q15898;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DI 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE (Clone XP6AllIB) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32078; AAA73888.1; -;
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 938 MW; 34841580477845BB CRC64;

Query Match 60.0%; Score 3; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e-05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4

Db 1 ESY 3

RESULT 2

Q9R3X0 PRELIMINARY; PRT; 8 AA.
ID Q9R3X0
AC Q9R3X0;

DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
 DE (Fragment).
 GN RBCL.
 OS Planktothrix rubescens.
 OC Bacteria; Cyanobacteria; Oscillatoriales; Planktothrix.
 OX NCBI_TaxID=59512;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BC-PLA 9316, and BC-PLA 9303;
 RX MEDLINE=20005589; PubMed=10537197;
 RA Beard S.J., Handley B.A., Hayes P.K., Walsby A.E.;
 RT "The diversity of gas vesicle genes in Planktothrix rubescens from
 RT Lake Zurich.";
 RL Microbiology 145:2757-2768(1999).
 DR EMBL; AJ132249; CAB59537.1; -.
 DR EMBL; AJ132248; CAB59534.1; -.
 FT NON_TER 1 1
 FT SEQUENCE 8 AA; 957 MW; 33D1AAA685BB19CB CRC64;
 SQ

Query Match 40.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
 Db 3 ES 4

RESULT 3

P72221
 ID P72221 PRELIMINARY; PRT; 8 AA.
 AC P72221;
 DT 01-FEB-1997 (TReMBLrel. 02, Created)
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Alginatase lyase (Fragment).
 GN ALX.
 OS Pseudomonas sp. (strain OS-ALG-9).
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=86038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OS-ALG-9;
 RA Fujiyama K.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OS-ALG-9;
 RX MEDLINE=93329366; PubMed=8336113;
 RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
 RT "Cloning, sequence analysis and expression in Escherichia coli of a
 RT gene encoding an alginatase lyase from Pseudomonas sp. OS-ALG-9.";
 RL J. Gen. Microbiol. 139:987-993(1993).
 DR EMBL; D38469; BRA21704.1; -.
 KW Lyase.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 841 MW; 461DDDC5A5B041B3 CRC64;
 SQ

Query Match 40.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
 Db 1 YT 2

RESULT 4

Q9Y4J4

ID Q9Y4J4 PRELIMINARY; PRT; 8 AA.
 AC Q9Y4J4;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
 DE (Fragment).
 GN Runt/82nt/MTG8 protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95002916; PubMed=7919324;
 RA Tighe J.E., Calabi F.;
 RT "Alternative, out-of-frame runt/MTG8 transcripts are encoded by the
 RT derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
 RT M2.";
 RL Blood 84:2115-2121(1994).
 DR EMBL; S74092; AAD14144.1; -.
 FT NON_TER 1 1
 FT SEQUENCE 8 AA; 1067 MW; 20F414044B17244B CRC64;
 SQ

Query Match 40.0%; Score 2; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
 Db 3 LE 4

RESULT 5

Q9Y4J3
 ID Q9Y4J3 PRELIMINARY; PRT; 8 AA.
 AC Q9Y4J3;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DE Runt/68nt/MTG8 protein (Fragment).
 GN Runt/68nt/MTG8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=95002916; PubMed=7919324;
 RA Tighe J.E., Calabi F.;
 RT "Alternative, out-of-frame runt/MTG8 transcripts are encoded by the
 RT derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
 RT M2.";
 RL Blood 84:2115-2121(1994).
 DR EMBL; S74094; AAD14973.2; -.
 FT NON_TER 1 1
 FT SEQUENCE 8 AA; 929 MW; 30B7644405B17244B CRC64;
 SQ

Query Match 40.0%; Score 2; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
 Db 3 LE 4

RESULT 6

O60773
 ID O60773 PRELIMINARY; PRT; 8 AA.
 AC O60773;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

```

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE FF126G10.1 (Parvalbumin) (Fragment).
GN PVALB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ho S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z82184; CAB05099.3; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 853 MW; 9BBB1DC2C731B5B9 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
Db 7 ES 8

RESULT 7
Q94623
ID Q94623 PRELIMINARY; PRT; 8 AA.
AC Q94623;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE MSUSP-2 protein (Fragment).
GN USP.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RA Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
RL Identification and mRNA developmental profiles of two ultraspiracle
RT isoforms in the epidermis and wings of Manduca sexta.;
RL Insect Mol. Biol. 6:41-53(1997).
DR EMBL; U57921; AAB64235.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 892 MW; F165BB0415A76B16 CRC64;

Query Match 40.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
Db 6 ES 7

RESULT 8
Q9XSY1
ID Q9XSY1 PRELIMINARY; PRT; 8 AA.
AC Q9XSY1;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE Retinoblastoma protein (Fragment).
GN RBL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=97049323; PubMed=8894053;
RA Venta P.J., Brouillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;
RT "Gene-specific universal mammalian sequence-tagged sites: application
to the canine genome.";
RL Biochem. Genet. 34:321-341(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Venta P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.;
RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (RBL)
gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF155737; AAD38807.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 895 MW; 1425BB18676721E3 CRC64;

Query Match 40.0%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
Db 6 ES 7

RESULT 9
Q8W8G2
ID Q8W8G2 PRELIMINARY; PRT; 8 AA.
AC Q8W8G2;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema savignyi (Longspine black urchin).
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematoidea;
OC Diadema.
OX NCBI_TaxID=105360;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DP751, SA2, SA7, SA10, GSA1, GSA3, GSA4, DOK17, and DOK105;
RT MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessling B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
DR EMBL; AY013065; AAL3860.1; -.
DR EMBL; AY013080; AAL3861.1; -.
DR EMBL; AY013083; AAL3862.1; -.
DR EMBL; AY013086; AAL3863.1; -.
DR EMBL; AY013088; AAL3864.1; -.
DR EMBL; AY013090; AAL3866.1; -.
DR EMBL; AY013091; AAL3867.1; -.
DR EMBL; AY013102; AAL3868.1; -.
DR EMBL; AY013103; AAL3869.1; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1037 MW; 701R173B46DDC2D3 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
Db 6 LE 7

RESULT 10
Q8W8G4

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ID	Q8W8G4	PRELIMINARY:	PRT:	8 AA.
AC	Q8W8G4:			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	Cytochrome oxidase subunit II (Fragment).			
GN	CoII.			
OS	Diadema mexicanum.			
OC	Diadematidae.			
OC	Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;			
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;			
OC	NCBI_TaxID=105359;			
OC	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C15, D3, D5, D6, CC56, GL23, DML, DM3, and DM71;			
RC	MEDLINE=21561594; PubMed=11703875;			
RC	Lessios H.A., Garrido M.J., Kessing B.D.;			
RA	"Demographic history of Diadema antillarum, a keystone herbivore on Caribbean reefs.";			
RT	Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).			
DR	EMBL; AY012908; AAL33837.1; -			
DR	EMBL; AY012911; AAL33838.1; -			
DR	EMBL; AY012913; AAL33839.1; -			
DR	EMBL; AY012914; AAL33840.1; -			
DR	EMBL; AY012919; AAL33842.1; -			
DR	EMBL; AY012940; AAL33847.1; -			
DR	EMBL; AY012949; AAL33849.1; -			
DR	EMBL; AY012950; AAL33850.1; -			
DR	EMBL; AY012951; AAL33851.1; -			
KW	Mitochondrion.			
FT	NON_TER 1			
SQ	SEQUENCE 8 AA; 1037 MW; 701B173B46DDC2D3 CRC64;			
Query Match 40.0%; Score 2: DB 8; Length 8;				
Best Local Similarity 100.0%; Pred.No. 8.3e+05;				
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gap				
QY	1 LE 2			
DB	11			
DB	6 LE 7			
RESULT 11				
Q8W8G6				
ID	Q8W8G6	PRELIMINARY:	PRT:	8 AA.
AC	Q8W8G6;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	Cytochrome oxidase subunit II (Fragment).			
GN	CoII.			
OS	Diadema mexicanum.			
OC	Diadematidae.			
OC	Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;			
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;			
OC	NCBI_TaxID=105359;			
OC	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=GLA121, and GLA124;			
RC	MEDLINE=21323357; PubMed=11430556;			
RA	Lessios H.A., Kessing B.D., Pearse J.S.;			
RA	"Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema.";			
RT	Phylogeography of the sea urchin Diadema.";			

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 2 SY 3

RESULT 15

Q8WFR5 ID Q8WFR5 PRELIMINARY; PRT; 8 AA.
AC Q8WFR5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema paucispinum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;
OC Diadema.
OX NCBI_TaxID=145530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HI1;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
DR EMBL; AY012959; AAL33852.1;
DR EMBL; AY012959; AAL33852.1;
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA; 954 MW; C41B173B46DDC2CE CRC64;

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
DB 6 LE 7

Search completed: September 24, 2003, 16:45:20
Job time : 49.75 secs

RESULT 13

Q8W8G3 ID Q8W8G3 PRELIMINARY; PRT; 8 AA.
AC Q8W8G3;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema paucispinum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;
OC Diadema.
OX NCBI_TaxID=145530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HI2, HI3, HI5, HI6, HI9, HI15, and HI19;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
DR EMBL; AY012960; AAL33853.1;
DR EMBL; AY012961; AAL33854.1;
DR EMBL; AY012962; AAL33855.1;
DR EMBL; AY012963; AAL33856.1;
DR EMBL; AY012964; AAL33857.1;
DR EMBL; AY012965; AAL33858.1;
DR EMBL; AY012966; AAL33859.1;
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA; 1037 MW; 701B173B46DDC2D3 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
DB 6 LE 7

RESULT 14

Q34909 ID Q34909 PRELIMINARY; PRT; 8 AA.
AC Q34909;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome b (Fragment).
OS Locusta migratoria (Migratory locust).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88223478; PubMed=2836084;
RA McCracken A., Uhlenbusch I., Gellissen G.;
RT "Structure of the cloned Locusta migratoria mitochondrial genome:
restriction mapping and sequence of its ND-1(URF-1) gene.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL; X05286; CAA28905.1;
KW Mitochondrion.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 1019 MW; F8B33723304B45B6 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 8;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:32:04 ; search time 11.25 seconds
(without alignments)
20.901 Million cell updates/sec

File: US-09-647-749A-1

Perfect score: 5

Sequence: 1 LESVT 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 369

Minimum DB seq length: 4

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2	40.0	5	1 PSK_DAUCA	P58261 daucus caro
2	2	40.0	7	1 HY7_PIG	P01153 sus scrofa
3	2	40.0	7	1 IGAO_DACDE	P06294 dactylium d
4	2	40.0	8	1 AL16_CARMA	P81819 carcinus ma
5	2	40.0	8	1 UPAL_HUMAN	P30087 homo sapien
6	2	40.0	9	1 FIBB_MACFU	P19345 macaca fusc
7	2	40.0	9	1 PGLR_DIAAB	P81179 diaprepes a
8	2	40.0	9	1 UHR2_HUMAN	P40929 homo sapien
9	2	40.0	9	1 ULAE_HUMAN	P31931 homo sapien
10	2	40.0	9	1 ULAE_HUMAN	P31934 homo sapien
11	2	40.0	9	1 UN19_CLOPA	P81355 clostridium
12	2	40.0	10	1 AMPN_HELAM	P81731 helioverpa
13	2	40.0	10	1 CA12_LITCI	P82086 litoria cit
14	2	40.0	10	1 CABR_LITXA	P56264 litoria xan
15	2	40.0	10	1 GON1_ALIMI	P37041 alligator m
16	2	40.0	10	1 GON1_PETWA	P20367 petromyzon
17	2	40.0	10	1 GON3_ONCKE	P04378 oncorhynch
18	1	20.0	4	1 EOSI_HUMAN	P02731 homo sapien
19	1	20.0	4	1 FAR3_HIRME	P42562 hirudo medi
20	1	20.0	4	1 FARA_HIRME	P42563 hirudo medi
21	1	20.0	4	1 FLRF_HIRME	P42561 hirudo medi
22	1	20.0	4	1 FLRN_ANTEL	P58707 anthopleura
23	1	20.0	4	1 FYRI_ANTEL	P58706 anthopleura
24	1	20.0	4	1 OCP3_OCTMI	P58649 octopus min
25	1	20.0	4	1 RM01_YEAST	P36515 saccharomyc
26	1	20.0	4	1 TUFT_HUMAN	P01858 homo sapien
27	1	20.0	5	1 AL14_CARMA	P81817 carcinus ma
28	1	20.0	5	1 B10A_CITFR	P13071 citrobacter
29	1	20.0	5	1 B10B_CITFR	P12997 citrobacter
30	1	20.0	5	1 E104_LITRU	P82100 litoria rub
31	1	20.0	5	1 FARP_ARTTR	P41853 artiposthi
32	1	20.0	5	1 PRC1_FERAM	P01373 periplaneta
33	1	20.0	5	1 RE21_LITRU	P82071 litoria rub

34	1	20.0	5	1 RE31_LITRU	P82072 litoria rub
35	1	20.0	5	1 RE32_LITRU	P82073 litoria rub
36	1	20.0	5	1 TRM3_ECOLI	P13973 escherichia
37	1	20.0	5	1 UC22_MAIZE	P80628 zea mays (m
38	1	20.0	5	1 UXA4_CHLTR	P38005 chlamydia t
39	1	20.0	6	1 ACPH_RABIT	P25154 oryctolagus
40	1	20.0	6	1 ASP2_IACSN	P82655 lactobacill
41	1	20.0	6	1 CIP1_MYTED	P13736 mytilus edu
42	1	20.0	6	1 LOK1_LOGMI	P41491 locusta mig
43	1	20.0	6	1 OVM_LEPDE	P42985 leptonotars
44	1	20.0	6	1 TRMF_SARBU	P41495 sarcophaga
45	1	20.0	6	1 TRP1_PSEBU	P36414 pseudomonas

ALIGNMENTS

RESULT 1
PSK_DAUCA
ID PSK_DAUCA STANDARD; PRT; 5 AA.
AC P58261:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
DE beta)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC STRAIN=cy. US-Harunakigosun.
RX MEDLINE=20212743; PubMed=10750705;
RA Hanai H., Matsuo T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA Kamada H., Sakagami Y.;

RT "A secreted peptide growth factor, phytosulfokine, acting as a stimulatory factor of carrot somatic embryo formation.";
RL Plant Cell Physiol. 41:27-32(2000).
CC -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC EMBRYOS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 3 3 SULFATION.
SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B300000 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YT 5
DB 3 YT 4

RESULT 2
HY7_PIG
ID HY7_PIG STANDARD; PRT; 7 AA.
AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Hypothalamic heptapeptide.
OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.-C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA Saifan M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus.";
RL Horm. Metab. Res. 13:228-232(1981).
DR PIR; A01417; NYPG7.
SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 5 SY 6

RESULT 3
IGAO_DACDE STANDARD; PRT; 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
OX NCBI_TaxID=5132;
RN [1]
RP SEQUENCE.
RA Avigad G., Markus Z.;
RT "Identification of a peptide inhibitor of galactose oxidase from
RT Dactylium dendroides.";
RL Fed. Proc. 31:447-447(1972).
CC -1- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE
CC GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
CC BINDING TO ITS PROSTHETIC COPPER GROUP.
DR PIR; A01341; XEYDGD.
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
DB 6 ES 7

RESULT 4
AL16_CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,

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RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD.RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 5 SY 6

RESULT 5
UPAL_HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RA MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1 1
FT UNSURE 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
DB 3 ES 4

RESULT 6
FIBB_MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.

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RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Pithecia patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT quonons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR: C24180; C24180.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1038 MW; 69FB65B9C735BB1B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
Db 3 ES 4

RESULT 7
PGLR_DIAAB STANDARD; PRT; 9 AA.
ID PGLR_DIAAB
AC P81179;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-polygalacturonase (PG) (EC 3.2.1.15) (Fragment).
OS Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;
OC Phytophaga; Curculionidae; Entiminae; Entimini; Diaprepes.
OX NCBI_TaxID=13040;
RN [1]
RP SEQUENCE.
RC TISSUE=Larval gut;
RA Doostdar H., McCallum T.G., Mayer R.T.;
RT "Purification and characterization of an endo-polygalacturonase from
RT the gut of West Indies sugarcane rootstalk borer weevil (Diaprepes
RT abbreviatus L.) larvae.";
RL Comp. Biochem. Physiol. 118B:861-867(1997).
CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -!- INDUCTION: INHIBITED BY CITRUS PGIP.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 9.4, ITS MW IS: 44.5 kDa.
CC -!- SIMILARITY: WEAK, TO OTHER POLYGALACTURONASES.
KW Hydrolase; Glycosidase; Cell wall.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1041 MW; 1F49087042DB41BB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
Db 2 YT 3

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RESULT 8
UHA2_HUMAN STANDARD; PRT; 9 AA.
ID UHA2_HUMAN
AC P40929;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1104 MW; 8874B1BB5B01B2CA CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
Db 6 YT 7

RESULT 9
ULAE_HUMAN STANDARD; PRT; 9 AA.
ID ULAE_HUMAN
AC P31931;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 115) (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquall C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 11 kDa.
DR SWISS-2DPAGE; P31931; HUMAN.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1096 MW; 477B3B173AE729C7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
Db 6 LE 7

RESULT 10
ULAH_HUMAN STANDARD; PRT; 9 AA.
ID ULAH_HUMAN
AC P31934;

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DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 94) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P31934; HUMAN.
FT NON_TER 1 3
FT VARIANT 3 3 A -> L
FT NON_TER 9 9 /FTID=VAR_000001.
FT SEQUENCE 9 AA; 990 MW; F1C07B172AB6DDCA CRC64;
SQ
Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LE 2
DB 6 LE 7
RESULT 11
UN19_CLOPA STANDARD; PRT; 9 AA.
AC P81355;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 19 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengstad R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998)
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.5, ITS MW IS: 38.0 kDa.
FT VARIANT 8 9 M -> D.
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1128 MW; E33E9B0AF5BB19DA CRC64;
SQ
Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ES 3
DB 4 ES 5
RESULT 12
AMPN_HELAM STANDARD; PRT; 10 AA.
ID AMPN_HELAM
AC P81731;

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DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Aminopeptidase N (EC 3.4.11.2) (CryIA(C) receptor) (Fragment).
OS Helicoverpa armigera (Cotton bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=29058;
RN [1]
RP SEQUENCE.
RC TISSUE=Midgut;
RX Ingle S.S., Trivedi N., Prasad R., Rao K.K., Chatpat H.S.;
RA "Aminopeptidase-N as a receptor for Bacillus thuringiensis CryIAC
RT toxin from Helicoverpa armigera.";
RL Submitted (MAR-1999) to the SWISS-PROT data bank.
CC -|- FUNCTION: ACTS AS A RECEPTOR FOR B.THURINGIENSIS TOXIN CRYIAC.
CC -|- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
CC Xbb- from a peptide, amide or arylamide. Xaa is preferably Ala, but
CC may be most amino acids including Pro (slow action). When a
CC terminal hydrophobic residue is followed by a prolyl residue, the
CC two may be released as an intact Xaa-Pro dipeptide.
CC -|- COFACTOR: Binds 1 zinc ion (By similarity).
CC -|- SIMILARITY: Belongs to peptidase family M1.
CC InterPro: IPR006025; Zs_M1peptidse.
DR PROSITE; PS00142; ZINC_PROTEASE; PARTIAL.
KW Hydrolase; Metalloprotease; Aminopeptidase; Zinc.
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1093 MW; 05042EB87B1F1FB CRC64;
SQ
Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YT 5
DB 3 YT 4
RESULT 13
CA12_LITCI STANDARD; PRT; 10 AA.
ID CA12_LITCI
AC P82086;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caerulein 1.2/1.2v4.
OS Litoria citropa (Australian blue mountains tree frog), and
OS Litoria splendida (Magnificent tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770; 30345;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEINS 1.2 AND 1.2v4).
RC SPECIES=L.citropa; TISSUE=skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
RC SPECIES=L.splendida; TISSUE=skin secretion;
RX MEDLINE=20059371; PubMed=10601876;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT "Differences in the skin peptides of the male and female Australian
RT tree frog Litoria splendida. The discovery of the aquatic male sex
RT pheromone splendorpherin, together with Phe8 caerulein and the
RT antibiotic peptide caerin 1.10.";
RL Eur. J. Biochem. 267:269-275(2000).
CC -|- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).

```

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- FM: Isoform 1.2Y4 differs from isoform 1.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1306 MW; 99DBFCD37861BB5A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
DB 4 YT 5

RESULT 14
CAER_LITXA STANDARD; PRT; 10 AA.
AC P56264;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caerulein.
OS Litoria xanthomera (Orange-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=79697;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinbörner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
RA Ramsay S.L.;
RT "New caerin antibacterial peptides from the skin glands of the
RT Australian tree frog Litoria xanthomera.";
RL J. Pept. Sci. 3:181-185(1997)
CC -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1354; METHOD=FAB.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; 1.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1290 MW; 99DBF3637861BB5A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
DB 4 YT 5

RESULT 15
GONL_ALLMI STANDARD; PRT; 10 AA.
ID GONL_ALLMI
AC P37041; P20407;

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DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Conadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
DE (Luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR: A60066; BHA01.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 4 SY 5

Search completed: September 24, 2003, 16:43:15
Job time : 12.25 secs

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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:39:35 ; Search time 20.4167 Seconds
(without alignments)
23.552 Million cell updates/sec

Title: US-09-647-749a-1

Perfect score: 5
Sequence: 1 LESYT 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1077

Minimum DB seq length: 4
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : PIR76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	60.0	9	2 PT0315	Ig heavy chain CRD
2	3	60.0	9	2 PT0324	Ig heavy chain CRD
3	2	40.0	4	2 A37832	phenol 2-monooxyge
4	2	40.0	5	2 B37832	ribosomal protein
5	2	40.0	5	2 B37832	ribosomal protein
6	2	40.0	5	2 B37832	ribosomal protein
7	2	40.0	5	2 B37832	ribosomal protein
8	2	40.0	5	2 B37832	ribosomal protein
9	2	40.0	5	2 B37832	ribosomal protein
10	2	40.0	5	2 B37832	ribosomal protein
11	2	40.0	5	2 B37832	ribosomal protein
12	2	40.0	5	2 B37832	ribosomal protein
13	2	40.0	5	2 B37832	ribosomal protein
14	2	40.0	5	2 B37832	ribosomal protein
15	2	40.0	5	2 B37832	ribosomal protein
16	2	40.0	5	2 B37832	ribosomal protein
17	2	40.0	5	2 B37832	ribosomal protein
18	2	40.0	5	2 B37832	ribosomal protein
19	2	40.0	5	2 B37832	ribosomal protein
20	2	40.0	5	2 B37832	ribosomal protein
21	2	40.0	5	2 B37832	ribosomal protein
22	2	40.0	5	2 B37832	ribosomal protein
23	2	40.0	5	2 B37832	ribosomal protein
24	2	40.0	5	2 B37832	ribosomal protein
25	2	40.0	5	2 B37832	ribosomal protein
26	2	40.0	5	2 B37832	ribosomal protein
27	2	40.0	5	2 B37832	ribosomal protein
28	2	40.0	5	2 B37832	ribosomal protein
29	2	40.0	5	2 B37832	ribosomal protein

fibrinogen beta ch
Ig heavy chain CDR
Ig heavy chain CRD
Ig heavy chain CRD
macrophage cytotox
alpha-2-macroglobu
collagen alpha 2(V
cytokeratin 4 - bo
fructose-bisphosph
3-oxoacid CoA-tran
Ig heavy chain V r
T-cell receptor ga
T-cell receptor be
hypothetical prote
gonadoliberin - pi
gonadoliberin - sh

ALIGNMENTS

RESULT 1
PT0315

Ig heavy chain CRD3 region (clone 6-109) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0315
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0315
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 60.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
DB 5 LES 7

RESULT 2
PT0324

Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0324
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0324
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 60.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4
DB 6 ESY 8

RESULT 3
A37832

```

phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragment)
C:Species: Pseudomonas sp.
C>Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993
C:Accession: A37832
R:Powlowski, J.; Shingler, V.
J. Bacteriol. 172, 6834-6840, 1990
A:Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxylase
A:Reference number: A37832; MUID:91072231; PMID:2254259
A:Accession: A37832
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <PO>
C:Keywords: oxidoreductase

Query Match          40.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
   ||
Db 1 SY 2

RESULT 4
I39964
ribosomal protein S4 - Bacillus circulans (fragment)
C:Species: Bacillus circulans
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39964
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
A:Accession: I39964
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99041; NID:g143471
C:Genetics:
A:Gene: rpsD

Query Match          40.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
   ||
   ||
Db 4 YT 5

RESULT 5
I39966
ribosomal protein S4 - Bacillus licheniformis (fragment)
C:Species: Bacillus licheniformis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39966
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
A:Accession: I39966
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99043; NID:g143475
C:Genetics:
A:Gene: rpsD

Query Match          40.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
   ||
   ||
Db 4 YT 5

RESULT 6
I39965
ribosomal protein S4 - Bacillus megaterium (fragment)
C:Species: Bacillus megaterium
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39965
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
A:Accession: I39965
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99042; NID:g143473
C:Genetics:
A:Gene: rpsD

Query Match          40.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
   ||
   ||
Db 4 YT 5

RESULT 7
I40469
dnaX-like protein - Bacillus subtilis (fragment)
C:Species: Bacillus subtilis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I40469
R:Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
Mol. Gen. Genet. 215, 478-482, 1989
A:Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
A:Reference number: I40469; MUID:89218958; PMID:2468993
A:Accession: I40469
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: EMBL:X14796; NID:g40130; PID:CAA32902.1; PID:g4376204
C:Genetics:
A:Start codon: GTG

Query Match          40.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
   ||
   ||
Db 2 SY 3

RESULT 8
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0308
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0308
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; Immunoglobulin

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Query Match 40.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
 DB 3 ES 4

RESULT 9
 JT0520
 Ig kappa chain V-III region (SD1) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Aug-1996
 C:Accession: JT0520
 R:Anker, R.; Conley, M.E.; Pollok, B.A.
 J. Exp. Med. 169, 2109-2119, 1989
 A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
 A:Reference number: JT0511; MUID:89279157; PMID:278547
 A:Accession: JT0520
 A:Molecule type: mRNA
 A:Residues: 1-5 <ANK>
 A:Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
 A:Note: a stop codon terminates the sequence in the V region
 C:Keywords: heterotrimer; immunoglobulin
 F:1-5/Domain: V kappa region <VRES>

Query Match 40.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
 DB 2 ES 3

RESULT 10
 PT0610
 T-cell receptor beta chain V-D-J region (100-2E) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0610
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0610
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FEE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
 DB 4 ES 5

RESULT 11
 JT0870
 Phytosulfokine alpha - garden asparagus (fragment)
 C:Species: Asparagus officinalis (garden asparagus)
 C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 19-Apr-2002
 C:Accession: JT0870
 R:Matsubayashi, Y.; Sakagami, Y.
 Proc. Natl. Acad. Sci. U.S.A. 93, 7623-7627, 1996
 A:Title: Phytosulfokine, sulfated peptides that induce the proliferation of single mesoderm cells
 A:Reference number: JT0870

A:Accession: JT0870
 A:Molecule type: protein
 A:Residues: 1-5 <MAT>

Query Match 40.0%; Score 2; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
 DB 3 YT 4

RESULT 12
 T11779
 phosphoglycerate transport regulatory protein pgTA - Salmonella typhimurium (fragment)
 C:Species: Salmonella typhimurium
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: T11779
 R:Yang, Y.L.; Goldrick, D.; Hong, J.S.
 J. Bacteriol. 170, 4299-4303, 1988
 A:Title: Identification of the products and nucleotide sequences of two regulatory genes
 A:Reference number: Z17339; MUID:86314933; PMID:2842311
 A:Accession: T11779
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <YAN>
 A:Cross-references: EMBL:M21279; NID:g858752; PID:g154260
 A:Experimental source: strain LT2

Query Match 40.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
 DB 2 LE 3

RESULT 13
 A31263
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
 C:Species: Plasmodium falciparum
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
 C:Accession: A31263
 R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
 A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
 A:Reference number: A94217; MUID:89057886; PMID:2904149
 A:Accession: A31263
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-6 <PET>
 C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
 DB 4 ES 5

RESULT 14
 B31263
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
 C:Species: Plasmodium falciparum
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
 C:Accession: B31263
 R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
 A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase

A;Reference number: A94217; MUID:89057886; PMID:2904149
 A;Accession: B31263
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-6 <PET>
 C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
 ||
 Db 4 ES 5

RESULT 15
 JH0784
 neuropeptide TE-6 - pig roundworm (fragment)
 C;Species: Ascaris suum (pig roundworm)
 C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 28-Apr-1995
 C;Accession: JH0784
 R;Smart, D.; Shaw, C.; Curry, W.J.; Johnston, C.F.; Thim, L.; Halton, D.W.; Buchanan, K.
 Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992
 A;Title: The primary structure of TE-6: a novel neuropeptide from the nematode Ascaris
 A;Reference number: JH0784; MUID:93038603; PMID:1417808
 A;Accession: JH0784
 A;Molecule type: protein
 A;Residues: 1-6 <SMA>
 A;Experimental source: gonoduct
 C;Keywords: neuropeptide

Query Match 40.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
 ||
 Db 5 LE 6

Search completed: September 24, 2003, 16:46:16
 Job time : 21.4167 secs

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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:45:30 ; Search time 32.9167 Seconds
(without alignments)
22.983 Million cell updates/sec

Title: US-09-647-749a-1

Perfect score: 5

Sequence: 1 LESY 5

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 566894 seqs, 151307093 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75270

Minimum DB seq length: 4

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Published Applications_AA:*

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- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	80.0	10	10	US-09-826-290-209
2	4	80.0	10	10	US-09-848-967-6
3	4	80.0	10	11	US-09-791-393-46
4	4	80.0	10	11	US-09-791-389-46
5	4	80.0	10	15	US-10-228-830-7
6	3	60.0	4	10	US-09-071-838-247
7	3	60.0	4	12	US-10-303-331-121
8	3	60.0	4	15	US-10-213-512-247
9	3	60.0	5	9	US-09-286-240-20
10	3	60.0	6	10	US-09-828-708-17
11	3	60.0	6	10	US-09-984-292-40
12	3	60.0	6	10	US-09-989-497-40
13	3	60.0	6	10	US-09-867-852-138
14	3	60.0	6	10	US-09-953-031A-8
15	3	60.0	6	10	US-09-995-225-47

16	3	60.0	6	12	US-09-995-225-47
17	3	60.0	6	12	US-10-227-110-7
18	3	60.0	6	12	US-10-190-082-144
19	3	60.0	6	12	US-10-162-435-44
20	3	60.0	6	12	US-10-321-807-129
21	3	60.0	6	15	US-10-097-175-99
22	3	60.0	6	15	US-10-262-832-2
23	3	60.0	7	9	US-09-126-559-4
24	3	60.0	7	9	US-09-845-667-7
25	3	60.0	7	9	US-09-873-676-95
26	3	60.0	7	10	US-09-770-002-6
27	3	60.0	7	10	US-09-884-767A-100
28	3	60.0	7	10	US-09-879-461-18
29	3	60.0	7	11	US-09-977-797A-38
30	3	60.0	7	11	US-09-563-222-6
31	3	60.0	7	11	US-09-563-222-33
32	3	60.0	7	11	US-09-759-112A-32
33	3	60.0	7	12	US-10-177-725-112
34	3	60.0	7	12	US-10-177-725-113
35	3	60.0	7	12	US-10-292-418-43
36	3	60.0	7	12	US-10-303-331-120
37	3	60.0	7	12	US-10-319-592-4
38	3	60.0	7	12	US-10-169-351-13
39	3	60.0	7	12	US-10-385-760-13
40	3	60.0	7	12	US-10-160-506-97
41	3	60.0	7	12	US-10-044-896-8
42	3	60.0	7	12	US-10-286-457-45
43	3	60.0	7	12	US-10-286-457-296
44	3	60.0	7	12	US-10-384-933-6
45	3	60.0	7	14	US-10-000-273-13

ALIGNMENTS

RESULT 1

US-09-826-290-209
; Sequence 209, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-209

Query Match 80.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 88;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
|||||
Db 3 LESY 6

RESULT 2

US-09-848-967-6
; Sequence 6, Application US/09848967
; Publication NO. US20020193295A1
; GENERAL INFORMATION:
; APPLICANT: CALENOFF, EMANUEL
; APPLICANT: DITLOW, CHARLES C.
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: 21417/92141
; CURRENT APPLICATION NUMBER: US/09/848,967
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 09/837,630
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-848-967-6

Query Match 80.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
|||||
Db 3 LESY 6

RESULT 3

US-09-791-393-46
; Sequence 46, Application US/09791393
; Publication NO. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-46

Query Match 80.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
|||||
Db 3 LESY 6

RESULT 4

US-09-791-389-46
; Sequence 46, Application US/09791389
; Publication NO. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-46

Query Match 80.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
|||||
Db 3 LESY 6

RESULT 5

US-10-228-830-7
; Sequence 7, Application US/10228830
; Publication NO. US20030100089A1
; GENERAL INFORMATION:
; APPLICANT: DuPont, Eric
; APPLICANT: Belliveau, Richard
; APPLICANT: Gingras, Denis
; APPLICANT: Renaud, Alain
; APPLICANT: Cadoret, France
; APPLICANT: Dimitriadou, Violetta
; APPLICANT: Falardeau, Pierre
; TITLE OF INVENTION: Serine Protease Inhibitor and Processes for the Preparation Th
; FILE REFERENCE: 32187.17
; CURRENT APPLICATION NUMBER: US/10/228,830
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/315,112
; PRIOR FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Squalus sp.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (5)..(9)
; OTHER INFORMATION: Xaa = Leucyl or Isoleucyl
US-10-228-830-7

Query Match 80.0%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYT 5

||||

Db 1 ESYT 4

RESULT 6

US-09-071-838-247
 ; Sequence 247, Application US/09071838
 ; Patent No. US20020152501A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer, Robert L.
 ; APPLICANT: Ohad, Nir
 ; APPLICANT: Kiyosue, Tomohiro
 ; APPLICANT: Yadegari, Ramin
 ; APPLICANT: Margossian, Linda
 ; APPLICANT: Harada, John
 ; APPLICANT: Goldberg, Robert B.
 ; TITLE OF INVENTION: Nucleic Acids That Control Seed and
 ; TITLE OF INVENTION: Fruit Development in Plants
 ; NUMBER OF SEQUENCES: 324
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/071.838
 ; FILING DATE: 01-MAY-1998
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bastiao, Kevin L.
 ; REGISTRATION NUMBER: 34,774
 ; REFERENCE/DOCKET NUMBER: 023070-086100US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 247:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-071-838-247

Query Match 60.0%; Score 3; DB 10; Length 4;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5

||||

Db 1 SYT 3

RESULT 7

US-10-303-121
 ; Sequence 121, Application US/10303331
 ; Publication No. US20030152976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Janssen, Giselle G.
 ; APPLICANT: Murray, Christopher J.
 ; APPLICANT: Winetzk, Deborah S.
 ; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
 ; FILE REFERENCE: GC617-3
 ; CURRENT APPLICATION NUMBER: US/10/303.331
 ; CURRENT FILING DATE: 2002-11-25

; PRIOR APPLICATION NUMBER: US 09/832,723
 ; PRIOR FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: US 60/197,259
 ; PRIOR FILING DATE: 2000-04-14
 ; NUMBER OF SEQ ID NOS: 125
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 121
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: consensus sequence
 ; US-10-303-331-121

Query Match 60.0%; Score 3; DB 12; Length 4;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3

||||

Db 1 LES 3

RESULT 8

US-10-213-512-247
 ; Sequence 247, Application US/10213512
 ; Publication No. US20030110536A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer, Robert L.
 ; APPLICANT: Ohad, Nir
 ; APPLICANT: Kiyosue, Tomohiro
 ; APPLICANT: Yadegari, Ramin
 ; APPLICANT: Margossian, Linda
 ; APPLICANT: Harada, John
 ; APPLICANT: Goldberg, Robert B.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
 ; TITLE OF INVENTION: Fruit Development in Plants
 ; FILE REFERENCE: 023070-086100US
 ; CURRENT APPLICATION NUMBER: US/10/213.512
 ; CURRENT FILING DATE: 2002-08-06
 ; PRIOR APPLICATION NUMBER: US/09/177,206
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: US 09/071,838
 ; PRIOR FILING DATE: 1998-05-01
 ; NUMBER OF SEQ ID NOS: 324
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 247
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis sp.
 ; US-10-213-512-247

Query Match 60.0%; Score 3; DB 15; Length 4;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5

||||

Db 1 SYT 3

RESULT 9

US-09-286-240-20
 ; Sequence 20, Application US/09286240
 ; Patent No. US20020010320A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pett, James W
 ; TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiotensin
 ; FILE REFERENCE: 10498/74073
 ; CURRENT APPLICATION NUMBER: US/09/286.240
 ; CURRENT FILING DATE: 1999-04-05
 ; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
US-09-286-240-20

Query Match 60.0%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5
|||
Db 1 SYT 3

RESULT 10
US-09-828-708-17
; Sequence 17, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-17

Query Match 60.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5
|||
Db 1 SYT 3

RESULT 11
US-09-984-292-40
; Sequence 40, Application US/09984292
; Patent No. US20020128433A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
US-09-984-292-40

Query Match 60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
|||
Db 3 LES 5

RESULT 12
US-09-989-497-40
; Sequence 40, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: N-terminal peptide sequence
US-09-989-497-40

Query Match 60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
|||
Db 3 LES 5

RESULT 13
US-09-867-852-138
; Sequence 138, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumitaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-138

Query Match 60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
|||
Db 3 LES 5

RESULT 14
US-09-953-031A-8
; Sequence 8, Application US/09953031A
; Patent No. US20020177177A1
; GENERAL INFORMATION:
; APPLICANT: Zwijsen, Renate
; TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
; FILE REFERENCE: 4238/80/13
; CURRENT APPLICATION NUMBER: US/09/953,031A
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 09/302,305
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(6)
; OTHER INFORMATION: Human cyclin D1 LXXXXL motif
US-09-953-031A-8

Query Match 60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
|||
Db 2 LES 4

RESULT 15
US-09-995-225-47
; Sequence 47, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Kuoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286

; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1e1 Sequence
US-09-995-225-47

Query Match 60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
|||
Db 2 LES 4

Search completed: September 24, 2003, 16:58:28
Job time : 33.9167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:40:45 ; Search time 16.6667 Seconds
(without alignments)
12.693 Million cell updates/sec

Title: US-09-647-749a-1

Perfect score: 5

Sequence: 1 LESYT 5

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 89050

Minimum DB seq length: 4

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/prodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	60.0	4	3	US-09-177-249-247
2	3	60.0	5	1	US-08-385-443-5
3	3	60.0	5	1	US-08-456-840-36
4	3	60.0	5	1	US-08-170-360-11
5	3	60.0	5	1	US-08-170-360-14
6	3	60.0	5	1	US-08-302-829-8
7	3	60.0	5	1	US-08-481-840A-6
8	3	60.0	5	1	US-08-266-407A-36
9	3	60.0	5	1	US-08-403-718-8
10	3	60.0	5	1	US-08-619-462-8
11	3	60.0	5	2	US-08-892-544-36
12	3	60.0	5	3	US-09-082-837A-8
13	3	60.0	5	3	US-09-421-845-8
14	3	60.0	5	4	US-09-298-924-35
15	3	60.0	5	6	5276016-4
16	3	60.0	5	6	5276016-8
17	3	60.0	5	6	5276016-10
18	3	60.0	5	6	5276016-11
19	3	60.0	6	1	US-07-859-291C-40
20	3	60.0	6	1	US-08-477-270-16
21	3	60.0	6	1	US-08-137-117D-137
22	3	60.0	6	2	US-08-436-717-137
23	3	60.0	6	2	US-08-436-065-3
24	3	60.0	6	2	US-08-702-673-4
25	3	60.0	6	2	US-08-893-853-44
26	3	60.0	6	2	US-08-310-912A-138
27	3	60.0	6	3	US-09-113-921-44

28	3	60.0	6	3	US-08-476-134A-33	Sequence 33, Appl
29	3	60.0	6	3	US-09-301-085-138	Sequence 138, App
30	3	60.0	6	4	US-09-302-305C-8	Sequence 8, Appli
31	3	60.0	6	4	US-08-757-425B-12	Sequence 12, Appl
32	3	60.0	6	4	US-08-757-425B-33	Sequence 33, Appl
33	3	60.0	6	4	US-09-451-067-44	Sequence 44, Appl
34	3	60.0	6	5	PCT-US93-01669-30	Sequence 30, Appl
35	3	60.0	6	5	PCT-US95-04589-138	Sequence 31, Appl
36	3	60.0	6	5	PCT-US95-04589-138	Sequence 138, App
37	3	60.0	6	6	5190920-6	Patent No. 5190920
38	3	60.0	6	6	5200320-15	Patent No. 5200320
39	3	60.0	6	6	5506208-6	Patent No. 5506208
40	3	60.0	7	1	US-08-201-046A-13	Sequence 13, Appl
41	3	60.0	7	1	US-08-076-092-33	Sequence 33, Appl
42	3	60.0	7	1	US-08-318-970B-16	Sequence 16, Appl
43	3	60.0	7	1	US-07-942-245-501	Sequence 501, App
44	3	60.0	7	2	US-08-483-636-18	Sequence 18, Appl
45	3	60.0	7	2	US-08-483-632-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-177-249-247
; Sequence 247, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-0861200S
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 247
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-247
Query Match 60.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 SYT 5
Db 1 SYT 3
RESULT 2
US-08-385-443-5
; Sequence 5, Application US/08385443
; Patent No. 5534495
; GENERAL INFORMATION:
; APPLICANT: PERT, CANDANCE B.
; APPLICANT: RUFF, MICHAEL R.
; TITLE OF INVENTION: TREATMENT OF NON-HTV NEUROPATHIC
; TITLE OF INVENTION: PAIN SYNDROMES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JULES E. GOLDBERG
; STREET: 261 MADISON AVENUE

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; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,443
; FILING DATE: 08-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/067,523
; FILING DATE: 23-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDBERG, JULES E.
; REGISTRATION NUMBER: 24,408
; REFERENCE/DOCKET NUMBER: ADVANCED PEPTIDES P5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-986-4090
; TELEFAX: 212-818-9479
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-385-443-5

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 3 SYT 5
Db 3 SYT 5

RESULT 3
US-08-456-840-36
; Sequence 36, Application US/08456840
; Patent No. 5597908
; GENERAL INFORMATION:
; APPLICANT: Taddei-Peters, W. C.
; APPLICANT: Butler, Sandra M.
; TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5597908el
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,840
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/266,407
; FILING DATE: 27-JUN-1994
; APPLICATION NUMBER: US 08/172,461
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
```

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; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-258-5200
; TELEFAX: 301-977-0847
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-840-36

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LES 3
Db 1 LES 3

RESULT 4
US-08-170-360-11
; Sequence 11, Application US/08170360
; Patent No. 5656602
; GENERAL INFORMATION:
; APPLICANT: Tseng, Albert P. S.
; APPLICANT: Inglis, Adam
; TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,360
; FILING DATE: 03-MAR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PCT/AU92/00333
; FILING DATE: 06-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 7058
; FILING DATE: 04-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1871-104A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-170-360-11

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYT 5
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Db 3 SYT 5

RESULT 5
US-08-170-360-14
; Sequence 14, Application US/08170360
; Patent No. 5656602
; GENERAL INFORMATION:
; APPLICANT: Tseng, Albert P. S.
; APPLICANT: Inglis, Adam
; TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,360
; FILING DATE: 03-MAR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: AU PCT/AU92/00333
; FILING DATE: 06-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 7058
; FILING DATE: 04-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1871-104A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-170-360-14

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 2 ESY 4
|||
Db 2 ESY 4

RESULT 6
US-08-302-829-8
; Sequence 8, Application US/08302829
; Patent No. 5756449
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Anders J
; APPLICANT: ASTON, Roger

; APPLICANT: CARLEN, Peter L
; APPLICANT: DOOB, Penelope R
; APPLICANT: MACFADDEN, Douglas K
; APPLICANT: PHIPPS, David J
; APPLICANT: RATHJEN, Deborah
; APPLICANT: WIDMER, Fred
; TITLE OF INVENTION: Peptide T and Related Peptides in the
; TREATMENT OF Inflammation, Including Multiple Sclerosis
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,829
; FILING DATE: 29-MAR-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00649
; FILING DATE: 29-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/987,674
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/915,118
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 645/92
; FILING DATE: 14-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/858,832
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26949
; REFERENCE/DOCKET NUMBER: 94,772
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-302-829-8

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 3 SYT 5
|||
Db 3 SYT 5

RESULT 7
US-08-481-840A-6
; Sequence 6, Application US/08481840A
; Patent No. 5763406
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Ove
; APPLICANT: MACFADDEN, D.
; TITLE OF INVENTION: Peptides for Treatment

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,840A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,777
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Iwanicki, John P
REGISTRATION NUMBER: 34,628
REFERENCE/DOCKET NUMBER: 93,741-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: peptide
US-08-481-840A-6
Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYT 5
Db 3 SYT 5
RESULT 8
US-08-266-407A-36
Sequence 36, Application US/08266407A
Patent No. 5786156
GENERAL INFORMATION:
APPLICANT: Taddei-peters, W. C.
APPLICANT: Butler, Sandra M.
TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5786156el
STREET: 1330 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,407A
FILING DATE: 27-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/172,461
FILING DATE: 21-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-258-5200
TELEFAX: 301-977-0847
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-266-407A-36
Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LES 3
Db 1 LES 3
RESULT 9
US-08-403-718-8
Sequence 8, Application US/08403718
Patent No. 5795858
GENERAL INFORMATION:
APPLICANT: MICHAELIS, JURGEN
APPLICANT: SLEIGH, MERILYN J.
TITLE OF INVENTION: TREATMENT OR PREVENTION OF CROHN'S
TITLE OF INVENTION: DISEASE AND/OR ULCERATIVE COLITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,718
FILING DATE: 31-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-74
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (704) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-403-718-8
Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYT 5
Db 3 SYT 5

RESULT 10
US-08-619-462-8
; Sequence 8, Application US/08619462
; Patent No. 5798335
; GENERAL INFORMATION:
; APPLICANT: MICHAELIS, JURGEN
; APPLICANT: Trigg, Timothy Elliot
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OR PREVENTION OF
; TITLE OF INVENTION: ECZEMA/DERMATITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,462
; FILING DATE: 07-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 47-84
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (704) 816-4100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-619-462-8

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5
Db 3 SYT 5

RESULT 11
US-08-892-544-36
; Sequence 36, Application US/08892544
; Patent No. 5874544
; GENERAL INFORMATION:
; APPLICANT: Taddei-Peters, W. C.
; APPLICANT: Butler, Sandra M.
; TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5874544el
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,544
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,407
; FILING DATE: 27-JUN-1994
; APPLICATION NUMBER: US 08/172,461
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-258-5200
; TELEFAX: 301-977-0847
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-892-544-36

Query Match 60.0%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
Db 1 LES 3

RESULT 12
US-09-082-837A-8
; Sequence 8, Application US/09082837A
; Patent No. 6011014
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Anders J
; APPLICANT: ASTON, Roger
; APPLICANT: CARLEN, Peter L
; APPLICANT: DOOB, Penelope R
; APPLICANT: MacFADDAEN, Douglas K
; APPLICANT: PHIPPS, David J
; APPLICANT: RATHJEN, Deborah
; APPLICANT: WIDMER, Fred
; TITLE OF INVENTION: Peptide T and Related Peptides in the Treatment of
; TITLE OF INVENTION: Inflammation, Including Multiple sclerosis
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,837A
; FILING DATE: 21-JUN-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,829
; FILING DATE: 29-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00649
; FILING DATE: 29-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/987,674
; FILING DATE: 09-DEC-1992


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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/915,118
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 645/92
; FILING DATE: 14-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/858,832
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Drehkoff, W. Dennis
; REGISTRATION NUMBER: 27193
; REFERENCE/DOCKET NUMBER: 94,772-A
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; US-09-082-837A-8

Query Match 60.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5
Db 3 SYT 5

RESULT 13
US-09-421-845-8
; Sequence 8, Application US/09421845
; Patent No. 6265374
; GENERAL INFORMATION:
; APPLICANT: Jorgensen
; APPLICANT: Aston
; APPLICANT: Carlen
; APPLICANT: Doob
; APPLICANT: MacFadden
; APPLICANT: Phipps
; APPLICANT: Rathjen
; APPLICANT: Widmer
; TITLE OF INVENTION: Peptide T and Related Peptides In the Treatment of
; TITLE OF INVENTION: Inflammation, Including Multiple Sclerosis.
; FILE REFERENCE: Peptide T Inflammation
; CURRENT APPLICATION NUMBER: US/09/421,845
; CURRENT FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/082,837
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-421-845-8

Query Match 60.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5
Db 3 SYT 5

RESULT 14
US-09-298-924-35
; Sequence 35, Application US/09298924
; Patent No. 6391595
; GENERAL INFORMATION:
; APPLICANT: KATO, Masaru
; APPLICANT: MIURA, Yutaka
; APPLICANT: KETOKU, Masako
; APPLICANT: IWAMATSU, Akihiro
; APPLICANT: KOBAYASHI, Kazuo
; APPLICANT: KOMEDA, Toshihiro
; TITLE OF INVENTION: NOVEL TRANSFERASE AND AMYLASE, PROCESS
; FOR PRODUCING THE ENZYMES, USE THEREOF, AND GENE CODING
; FOR THE SAME
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,924
; FILING DATE: 26-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,569
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 7-120673
; FILING DATE: 21-APR-1995
; APPLICATION NUMBER: JP 6-311185
; FILING DATE: 21-NOV-1994
; APPLICATION NUMBER: JP 6-286917
; FILING DATE: 21-NOV-1994
; APPLICATION NUMBER: JP 6-290394
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: JP 6-194223
; FILING DATE: 18-AUG-1994
; APPLICATION NUMBER: JP 6-133354
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 49441/110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
; US-09-298-924-35

Query Match 60.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
Db 3 LES 5

RESULT 15
5276016-4
; Patent No. 5276016
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; APPLICANT: PERT, CANDACE B.;RUFF, WILLIAM R.
; FARRAR,WILLIAM L.
; TITLE OF INVENTION: SMALL PEPTIDES WHICH INHIBIT
; BINDING TO T-4 RECEPTORS AND ACT AS IMMUNOGENS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/568,616
; FILING DATE: 16-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 314,507
; FILING DATE: 15-FEB-1989
; APPLICATION NUMBER: 48,148
; FILING DATE: 11-MAY-1987
; APPLICATION NUMBER: 878,586
; FILING DATE: 26-JUN-1986
; APPLICATION NUMBER: 869,919
; FILING DATE: 03-JUN-1986
; SEQ ID NO:4:
; LENGTH: 5
5276016-4
Query Match 60.0%; Score 3; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYT 5
Db 3 SYT 5
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Search completed: September 24, 2003, 16:47:03
Job time : 17.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:31:29 ; Search time 48.75 Seconds
(without alignments)
16.280 Million cell updates/sec

Title: US-09-647-749A-1

Perfect score: 5
Sequence: 1 LESYT 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 250473

Minimum DB seq length: 4
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	20	AA19695 HIV-1 gp120 induce
2	4	80.0	9	22	AA198253 Human peptide #152
3	4	80.0	9	24	ABR06127 Human cancer-relat
4	4	80.0	9	24	ABR06277 Human cancer-relat
5	4	80.0	9	24	ABR06530 Human cancer-relat
6	4	80.0	9	24	ABR06714 Human cancer-relat
7	4	80.0	9	24	ABR06735 Human cancer-relat
8	4	80.0	10	22	ABB55971 Vascular dementia-
9	4	80.0	10	22	ABB52194 Human API-148 try

10	4	80.0	10	22	AAU28456 DPL tryptic digest
11	4	80.0	10	22	AAU26102 Depression-Associat
12	4	80.0	10	23	ABG78790 Multiple sclerosis
13	4	80.0	10	24	ABP72727 Serine protein inh
14	4	80.0	10	24	ABR06184 Human cancer-relat
15	4	80.0	10	24	ABR06569 Human cancer-relat
16	4	80.0	10	24	ABR06767 Human cancer-relat
17	3	60.0	4	19	AAU20715 Human neurofilamen
18	3	60.0	4	19	AAU20656 Human neurofilamen
19	3	60.0	4	22	AAE08524 Peptide for analys
20	3	60.0	4	23	ABP67653 Human CD66 family
21	3	60.0	5	8	AAU71550 AIDS virus recepto
22	3	60.0	5	8	AAU71551 AIDS virus recepto
23	3	60.0	5	9	AAU83009 Blocking peptide u
24	3	60.0	5	10	AAU91855 Pentapeptide which
25	3	60.0	5	13	AAU26903 Herpes simplex vir
26	3	60.0	5	13	AAU28941 Example of a gener
27	3	60.0	5	14	AAU44339 Peptide T related
28	3	60.0	5	15	AAU47830 Peptide T for intr
29	3	60.0	5	15	AAU47831 Peptide T for intr
30	3	60.0	5	16	AAU77332 Human apolipoprote
31	3	60.0	5	16	AAU61485 Peptide T variant
32	3	60.0	5	16	AAU59490 Peptide T variant
33	3	60.0	5	17	AAU98997 Peptide T analogue
34	3	60.0	5	17	AAU90645 S. acidocaldarius
35	3	60.0	5	20	AAU90315 Human anti-idiotyp
36	3	60.0	5	21	AAU52187 Human anti-RBs ant
37	3	60.0	5	22	AAU9512 Immediate early ge
38	3	60.0	5	22	AAU67490 Human heavy chain
39	3	60.0	5	22	AAU37563 C98 beta chain rid
40	3	60.0	5	22	AAU55661 Monocyte surface r
41	3	60.0	5	22	AAU57508 Galectin 3 C-termi
42	3	60.0	5	22	AAU57918 Galectin 3 C-termi
43	3	60.0	5	23	ABP67642 Human CD66 family
44	3	60.0	5	23	ABU05140 T-cell surface rec
45	3	60.0	5	23	ABU63433 Monocyte surface r

ALIGNMENTS

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RESULT 1
AAU49695
ID AAU49695 standard; peptide; 5 AA.
XX
XX
AC AAU49695;
XX
XX
DT 18-JAN-2000 (first entry)
XX
XX
DE HIV-1 gp120 induced neuronal cell death inhibiting peptide #1.
XX
XX
KW Neurological degenerative disease; HIV-1; envelope protein; gp120;
KW toxic; neuron; accessory glial cell; chemokine; viral infection;
KW neuronal cell death; encephalopathy; neuropathy; memory loss;
KW dementia; depression; psychosis; opportunistic infection;
KW neurotoxicity; inflammatory neurological disease; multiple sclerosis;
KW tropical spastic paraparesis; Alzheimer's disease.
XX
OS Synthetic.
XX
XX
PN W09591254-A1.
XX
PD 14-OCT-1999.
XX
PF 06-APR-1999; 99WO-US07514.
XX
PR 06-APR-1998; 98US-0080836.
XX
PA (ADIM-) ADVANCED IMMUNIT INC.
XX
PI Pert C, Ruff M;
XX
WPI; 1999-633695/54.
```

XX PT New peptides useful for inhibiting human immuno-deficiency virus type 1
 PT (HIV-1) gp120 induced neuronal cell death -
 XX
 XX Claim 1; Page 11; 16pp; English.
 PS
 CC AAY49695 and AAY49696 represent peptides which inhibit HIV-1 gp120
 CC induced neuronal cell death. Pharmaceutical compositions containing the
 CC peptides are useful for treating symptoms caused by neuronal cell loss.
 CC Such conditions especially associated with HIV infection include
 CC encephalopathies, neuropathies, memory loss, dementia, depression,
 CC psychosis and opportunistic infections. The peptides act as antagonists
 CC of gp120-mediated neurotoxicity and subsequent neuronal degeneration.
 CC This enables therapeutic treatment of HIV infection and other
 CC inflammatory neurological diseases, including multiple sclerosis,
 CC tropical spastic paraparesis and Alzheimer's disease.
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 5; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LESYT 5
 Db 1 LESYT 5
 RESULT 2
 AAM98253
 ID AAM98253 standard; Peptide; 9 AA.
 AC
 XX AAM98253;
 AC
 XX 24-JAN-2002 (first entry)
 DT
 XX
 XX Human peptide #1528 encoded by a SNP oligonucleotide.
 DE
 XX
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiopeptin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 XX Homo sapiens.
 OS
 XX WO200147944-A2.
 PN
 XX 05-JUL-2001.
 PD
 XX 28-DEC-2000; 2000WO-US35498.
 PF
 XX 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 PR
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shinkets RA, Leach M;
 PI
 XX WPI; 2001-465210/50.
 DR
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PT
 XX Disclosure; Page 4003; 4143pp; English.
 PS
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiopeptin, apoptosis related proteins, cadherin, cyclin,

CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 XX

SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 LESY 4

Db 2 LESY 5

RESULT 3

ABR06127
 ID ABR06127 standard; Peptide; 9 AA.

XX

AC ABR06127;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 109P1D4 HLA peptide #62.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US11654.

XX

PR 10-APR-2001; 2001US-282739P.

XX

PR 10-APR-2001; 2001US-283112P.

XX

PR 25-APR-2001; 2001US-286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of

XX

PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX

PT diagnostic reagents for eliciting cellular or humoral immune response

XX

PT in cancer patients -

XX

PS Claim 13; Page 173; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.

XX SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYT 5
 ||||
Db 3 ESYT 6

RESULT 4

ABR06277
ID ABR06277 standard; Peptide; 9 AA.

XX AC ABR06277;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 109p1D4 HLA peptide #212.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of

XX PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX PT diagnostic reagents for eliciting cellular or humoral immune response

XX PT in cancer patients -

XX PS Claim 13; Page 175; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and

XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

XX CC proteins are useful for eliciting a humoral or cellular immune response.

XX CC The genes are useful as probes and primers for the amplification and/or

XX CC detection of genes, mRNAs or their fragments, as reagents for the

XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of

XX CC directing the expression of the protein, as tools for modulating or

XX CC inhibiting the expression of genes and/or translation of transcripts, and

XX CC as therapeutic agents. The proteins and peptides are useful as

XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present

XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX CC from the invention.

XX SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYT 5
 ||||
Db 3 ESYT 6

RESULT 5

ABR06530
ID ABR06530 standard; Peptide; 9 AA.

XX AC ABR06530;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 109p1D4 HLA peptide #465.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of

XX PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX PT diagnostic reagents for eliciting cellular or humoral immune response

XX PT in cancer patients -

XX PS Claim 13; Page 177; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and

XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

XX CC proteins are useful for eliciting a humoral or cellular immune response.

XX CC The genes are useful as probes and primers for the amplification and/or

XX CC detection of genes, mRNAs or their fragments, as reagents for the

XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of

XX CC directing the expression of the protein, as tools for modulating or

XX CC inhibiting the expression of genes and/or translation of transcripts, and

XX CC as therapeutic agents. The proteins and peptides are useful as

XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present

XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX CC from the invention.

XX SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYT 5

Db 2 ESYT 5

RESULT 6

ABR06714
ID ABR06714 standard; Peptide; 9 AA.

XX AC ABR06714;

XX	19-MAY-2003	(first entry)	
XX	DT		
XX	DE	Human cancer-related protein 109P1D4 HLA peptide #649.	
XX	DE		
XX	KW	Human; cytostatic; vaccine; cancer; immune response; HLA;	
KW	KW	human leukocyte antigen.	
XX	OS	Homo sapiens.	
XX	WO200283921-A2.		
XX	PN		
XX	PN		
XX	PD	24-OCT-2002.	
XX	PF		
XX	PF	10-APR-2002; 2002WO-US11654.	
XX	PR		
XX	PR	10-APR-2001; 2001US-282739P.	
XX	PR	10-APR-2001; 2001US-283112P.	
XX	PR	25-APR-2001; 2001US-286630P.	
XX	PA	(AGEN-) AGENSYS INC.	
XX	PA		
XX	PI	Jakovovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;	
XX	PI	Morrison K, Morrison RK, Raitano AB;	
XX	DR	WPI; 2003-075555/07.	
XX	DR		
XX	PT	New composition comprising a substance that modulates the structure of	
PT	PT	proteins and polynucleotides, useful for therapeutic, prognostic and	
PT	PT	diagnostic reagents for eliciting cellular or humoral immune response	
PT	PT	in cancer patients	
XX	PS		
XX	PS	Claim 13; Page 179; 102ipp; English.	
XX	CC		
XX	CC	The present invention relates to novel human cancer-related genes and	
XX	CC	proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and	
XX	CC	proteins are useful for eliciting a humoral or cellular immune response.	
XX	CC	The genes are useful as probes and primers for the amplification and/or	
XX	CC	detection of genes, mRNAs or their fragments, as reagents for the	
XX	CC	diagnosis and/or prognosis of cancer, as coding sequences capable of	
XX	CC	directing the expression of the protein, as tools for modulating or	
XX	CC	inhibiting the expression of genes and/or translation of transcripts, and	
XX	CC	as therapeutic agents. The proteins and peptides are useful as	
XX	CC	therapeutic, prognostic and diagnostic reagents for cancer. The present	
XX	CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example	
XX	CC	from the invention.	
XX	CC		
XX	SQ	Sequence 9 AA;	
	Query Match	80.0%; Score 4; DB 24; Length 9;	
	Best Local Similarity	100.0%; Pred. No. 9.3e+05;	
	Matches 4; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
Oy	2 ESYT 5		
Dd	2 ESYT 5		
RESULT 7			
ABR06735			
ID	ABR06735 standard; Peptide; 9 AA.		
XX	AC	ABR06735;	
XX	AC		
XX	DT	19-MAY-2003 (first entry)	
XX	DE	Human cancer-related protein 109PID4 HLA peptide #670.	
XX	DE		
XX	KW	Human; cytostatic; vaccine; cancer; immune response; HLA;	
KW	KW	human leukocyte antigen.	
XX	OS	Homo sapiens.	
OS	OS		

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX Herath HMAC, Parekh RB, Rohliff C;
XX WPI; 2001-557937/62.
XX
XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analysing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD -
XX
XX Claim 6; Page 33; 151pp; English.
XX
XX The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for
CC monitoring the effect of therapy administered to a subject having VD.
CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
XX useful for the treatment of VD and for gene therapy.
XX
XX Sequence 10 AA;
SQ

Query Match 80.0%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LESY 4
Db | | | |
3 LESY 6

RESULT 9
ABB52194
ID ABB52194 standard; Peptide; 10 AA.
XX
AC ABB52194;
XX
DT 08-FEB-2002 (first entry)
XX
DE Human API-148 tryptic digest peptide #2.
XX
XX Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
XX Homo sapiens.
XX
XX WO200175454-A2.
XX
XX 11-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US10908.
XX
XX 03-APR-2000; 2000US-194504P.
XX
XX 28-NOV-2000; 2000US-253647P.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFI2) PFIZER INC.
XX
XX Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;
PI Potter DM, Rohliff C, Silber BM, Stiger TR, Sunderland PI;
PI Townsend RR, White F, Williams SA;
XX
XX WPI; 2001-639384/73.

XX Screening for Alzheimer's disease in a mammal, by making
PT two-dimensional array of a feature whose relative abundance correlates
PT with disease, and comparing with abundance of the feature in samples of
PT healthy persons -
XX
XX Example; Page 30; 162pp; English.
XX
XX The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
CC serum or plasma. The abundance of the AFs and APIs is then
CC normalised to an Expression Reference Protein Isoform (ERPI) in
CC order to determine whether a patient is suffering from, or has
CC a predisposition to, Alzheimer's Disease. The relative abundance of
CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
XX The present sequence is a peptide produced from an API by proteolysis.
XX Sequence 10 AA;
SQ

Query Match 80.0%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LESY 4
Db | | | |
3 LESY 6

RESULT 10
AAU28456
ID AAU28456 standard; Peptide; 10 AA.
XX
AC AAU28456;
XX
DT 03-JAN-2002 (first entry)
XX
DE DPI tryptic digest peptide #53.
XX
XX Human; depression associated protein isoform; tryptic digest peptide;
KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
KW maniac-depressive illness; schizoaffective disorder.
XX
XX Homo sapiens.
XX
XX WO200162787-A1.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB00786.
XX
XX 24-FEB-2000; 2000GB-0004412.
XX
XX 08-DEC-2000; 2000GB-0030050.
XX
XX 12-DEC-2000; 2000US-0254830.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAC, Parekh RB, Rohliff C, Terrett JA, Tyson KL;
XX WPI; 2001-570626/64.
XX
XX Novel nucleic acid encoding a protein associated with bipolar affective
PT disorder, which is used for diagnosis, prophylaxis and therapy of
PT neuropsychiatric disorders, such as bipolar affective disorder -
XX
XX Disclosure; Page 31; 153pp; English.
XX
XX The present invention relates to the identification of depression
CC associated protein isoforms (DPIs), particularly the tryptic digest
CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
CC described are decreased in the cerebrospinal fluid (CSF) of BAD

CC (bipolar affective disorder) subjects, whilst other DPIs
 CC (AAU28626-AAU28887) are increased in BAD subjects. Also described
 CC are peptide sequences identified from DPI-45 and DPI-213 and the
 CC nucleic acid sequences they are encoded by. The sequences of the
 CC invention are useful for clinical screening, diagnosis, prognosis,
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
 CC known as bipolar mood disorder, BP), maniac-depressive illnesses,
 CC attention deficit disorders, schizoaffective disorders, and unipolar
 CC affective disorders. The present sequence represents one of the DPI
 CC tryptic digest peptides of the present invention.

SQ Sequence 10 AA;
 Query Match 80.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
 IIII
 Db 3 LESY 6

RESULT 11
 AAU26102
 ID AAU26102 standard; Peptide; 10 AA.
 XX AC AAU26102;
 XX DT 18-DEC-2001 (first entry)
 XX DE Depression-Associated Protein isoform DPI-12.
 XX Human: Bipolar Affective Disorder; BAD; Depression-Associated feature;
 KW DF: Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
 KW attention deficient disorder; schizoaffective disorder;
 KW unipolar affective disorder.
 XX OS Homo sapiens.
 XX WO200163294-A2.
 XX 30-AUG-2001.
 XX 23-FEB-2001; 2001WO-GB00791.
 XX 24-FEB-2000; 2000GB-0004412.
 XX 08-DEC-2000; 2000GB-0030050.
 XX 12-DEC-2000; 2000US-0254830.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX Herath HMAC, Parekh RB, Rohlf C;
 XX WPI; 2001-582081/65.
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD)
 XX or unipolar depression, or for screening for modulators, comprises a
 XX PT BAD-associated protein isoform -
 XX PS Claim 8; Page 31; 163pp; English.

CC The invention relates to a preparation comprising an isolated bipolar
 CC Affected disorder (BAD)-associated Protein Isoform (DPIs). The DPI's are
 CC used to screen, diagnose or prognose of BAD or unipolar depression,
 CC determine the stage or severity of BAD or unipolar depression, identify a
 CC subject at risk of developing BAD or unipolar depression, or monitor the
 CC effect of therapy in a subject. They are also used to screen for or
 CC identify agents that interact with a DPI. These agents, antibodies
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
 CC or prevent BAD or unipolar depression. Diseases that can be treated are
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
 CC unipolar affective disorder. The DPIs are used in proteomics. The

CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
 CC BAD or unipolar depression overcomes the problems of using gene
 CC expression analysis, such as not being able to obtain central nervous
 CC system (CNS) tissue from a living patient under normal circumstances.
 CC The present sequence is a DIP decreased in the CSF (cerebro-spinal
 CC fluid) of subjects having BAD.

SQ Sequence 10 AA;
 Query Match 80.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
 IIII
 Db 3 LESY 6

RESULT 12
 ABG78790
 ID ABG78790 standard; Peptide; 10 AA.
 XX AC ABG78790;
 XX DT 29-NOV-2002 (first entry)
 XX DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #278.
 XX KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;
 KW human; multiple sclerosis-associated protein isoform; MSPI;
 KW antiinflammatory; neuroprotective.
 XX OS Homo sapiens.
 XX WO200259604-A2.
 XX 01-AUG-2002.
 XX 25-JAN-2002; 2002WO-GB00330.
 XX 26-JAN-2001; 2001US-264404P.
 XX 20-NOV-2001; 2001US-331647P.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX Herath HMAC, Parekh RB, Rohlf C;
 XX WPI; 2002-599812/64.
 XX Screening or diagnosing multiple sclerosis (MS), useful for e.g.
 XX determining the stage or severity of MS, comprises detecting the
 XX presence of MS-associated features or protein isoforms by 2-dimensional
 XX electrophoresis -
 XX PS Disclosure; Page 31; 128pp; English.

CC This invention relates to a novel method for screening or diagnosing
 CC multiple sclerosis (MS) in a subject to determine the stage or severity
 CC of MS, to identify a subject at risk of developing MS or to monitor the
 CC effect of a therapy administered. The method comprises analysing a
 CC sample body fluid from the subject by two-dimensional electrophoresis
 CC and detecting the presence of multiple sclerosis-associated features
 CC (MSFs), or multiple sclerosis-associated protein isoforms (MSPIs).
 CC The MSF's of the invention correspond to spots identified on a 2D gel
 CC these proteins may have antiinflammatory or neuroprotective activity.
 CC The methods of the invention and the compositions are useful for
 CC clinical screening, diagnosis and treatment of MS, for monitoring the
 CC effectiveness of MS treatment, for selecting participants in clinical
 CC trials, for identifying patients most likely to respond to a particular
 CC therapeutic treatment and for screening and developing drugs for
 CC treatment of MS. Agents that modulate the expression or activity of an
 CC MSPI are useful for treating MS, for preventing or delaying the onset or
 CC development of MS, to prevent or delay the progression of MS, or to

CC ameliorate the symptoms MS. Nucleic acids comprising a sequence encoding
 CC an MSP1, MSP1-related polypeptide, or their fragments are useful for
 CC promoting MSP1 function by gene therapy. The present sequence represents
 CC a human multiple sclerosis associated feature tryptic digest
 CC peptide of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 4; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LESY 4
 Db 3 LESY 6
 RESULT 13
 ABP72727
 ID ABP72727 standard; Peptide; 10 AA.
 XX AC
 AC ABP72727;
 DT 11-JUN-2003 (first entry)
 XX Serine protein inhibitor p54 internal peptide fragment.
 DE
 XX Serine protease inhibitor; serpin; elastase; inhibitor; shark;
 KW cartilage; antiinflammatory; antipsoriatic; hepatotropic;
 KW cytostatic; antiarthritic; vasotropic; anticoagulant; thrombolytic;
 KW antiarteriosclerotic; antiallergic; dermatological; analgesic;
 KW vulnery; antiasthmatic; immunosuppressive; hypotensive.
 XX
 OS Squalus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5 /label= Leu, Ile
 FT FT
 FT Misc-difference 8 /label= Leu, Ile
 FT FT
 FT Misc-difference 9 /label= Leu, Ile
 FT FT
 FT /label= Leu, Ile
 PN WO2003018620-A2.
 XX
 XX 06-MAR-2003.
 PD
 XX 23-AUG-2002; 2002WO-CA01309.
 XX
 XX 27-AUG-2001; 2001US-315112P.
 PR
 XX (AETE-) LES LAB AETERNA INC.
 PA
 XX Dupont E, Bellevue R, Gingras D, Renaud A, Cadoret F;
 PI Dimitriadou V, Falardeau P;
 PI WPI: 2003-290045/28.
 XX
 XX New glycoprotein having an inhibitory activity towards elastolytic
 PT serine proteases, useful for preventing or treating diseases associated
 PT with excess levels of serine protease, e.g. inflammation, allergy,
 PT cancer or thrombosis -
 XX
 FS Claim 4; Page 22; 58pp; English.
 XX
 CC The present sequence is an internal peptide fragment of a novel
 CC shark cartilage protein, designated p54, that is a serpin-like
 CC glycoprotein having inhibitory activity towards elastolytic
 CC serine proteases. The peptide was obtained by tryptic digestion.
 CC p54 is a glycoprotein having an apparent molecular weight of 54 kDa
 CC (46 kDa for the proteinaceous backbone). A shark cartilage protein
 CC which comprises any of the peptides given in ABP72721-32, including
 CC the present sequence, is claimed, and also an antibody directed

CC against the protein, nucleic acids encoding any of the peptides,
 CC methods of detecting the anti-elastase serpin or its gene, and a
 CC method for obtaining a serine elastase inhibitor from cartilage.
 CC The p54 protein is useful in preventing, treating or alleviating the
 CC symptoms of disorders or diseases associated with an excess level
 CC of serine protease, such as inflammation, psoriasis, cancer, emphysema,
 CC pulmonary hypertension, liver fibrosis, cancer, arthritis,
 CC thrombosis, cystic fibrosis, cirrhosis, immune hypersensitivity,
 CC chronic bronchitis, atherosclerosis, vasculitis, rhinitis, nasal
 CC polyposis, dermatitis, colitis, pancreatitis, coronary artery
 CC spasms, cluster headaches, wounds or asthma (all claimed).
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ESYT 5
 Db 1 ESYT 4
 RESULT 14
 ABR06184
 ID ABR06184 standard; Peptide; 10 AA.
 XX AC ABR06184;
 AC ABR06184;
 DT 19-MAY-2003 (first entry)
 XX Human cancer-related protein 109PID4 HLA peptide #119.
 DE
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 KW Homo sapiens.
 OS
 XX WO200283921-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 10-APR-2002; 2002WO-US11654.
 XX
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 10-APR-2001; 2001US-283112P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 PI WPI: 2003-075555/07.
 DR
 XX New composition comprising a substance that modulates the structure of
 XX proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 PT
 XX Claim 13; Page 174; 1021pp; English.
 PS
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.
XX
SQ Sequence 10 AA;
Query Match 80.0%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ESYT 5
Db |||||
3 ESYT 6
Search completed: September 24, 2003, 16:42:41
Job time : 49.75 secs

RESULT 15
ABR06569
ID ABR06569 standard; Peptide; 10 AA.
XX
AC ABR06569;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 109PLD4 HLA peptide #504.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
PS Claim 13; Page 178; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
SQ Sequence 10 AA;
Query Match 80.0%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ESYT 5
Db |||||

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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:39:05 ; Search time 68.25 Seconds
(without alignments)
26.467 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7

Sequence: 1 IKEYFTS 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1349

Minimum DB seq length: 4

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organella:*
9: sp.phage:*
10: sp.plant:*
11: sp.priodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	42.9	8	Q9N6M5	Q9n6m5 toxoplasma
2	3	42.9	10	Q9NP06	Q9np06 homo sapien
3	3	42.9	10	Q9NP07	Q9np07 homo sapien
4	2	28.6	7	P72081	P72081 nocardia la
5	2	28.6	7	O8GL12	O8gl12 borrelia bu
6	2	28.6	7	O8GL04	O8gl04 borrelia bu
7	2	28.6	7	O8GL00	O8gl00 borrelia bu
8	2	28.6	8	Q9S6B5	Q9s6b5 escherichia
9	2	28.6	8	Q9R7T2	Q9r7t2 escherichia
10	2	28.6	8	Q8RJ10	Q8rj10 streptomyce
11	2	28.6	8	P77556	P77556 escherichia
12	2	28.6	8	Q56759	Q56759 xanthobacte
13	2	28.6	8	Q9R9E0	Q9r9e0 bacillus su
14	2	28.6	8	Q8G940	Q8g940 borrelia bu
15	2	28.6	8	P87225	P87225 saccharomyc
16	2	28.6	8	Q15893	Q15893 homo sapien

17	2	28.6	8	4	Q15888	Q15888 homo sapien
18	2	28.6	8	4	O8TF70	O8tf70 homo sapien
19	2	28.6	8	4	Q9H4D3	Q9h4d3 homo sapien
20	2	28.6	8	6	O18854	O18854 canis famli
21	2	28.6	8	6	Q95M23	Q95m23 sus scrofa
22	2	28.6	8	7	Q29810	Q29810 homo sapien
23	2	28.6	8	8	Q94VF6	Q94vf6 varanus job
24	2	28.6	8	8	O9TK55	O9tke5 leptospermu
25	2	28.6	8	8	Q34909	Q34909 locusta mig
26	2	28.6	8	10	Q9SAY7	Q9say7 discorea t
27	2	28.6	8	10	O8GTG5	O8gtg5 lycopersico
28	2	28.6	8	11	O9ET21	O9et21 mus musculu
29	2	28.6	8	11	O8R5M9	O8r5m9 mus musculu
30	2	28.6	8	12	O84273	O84273 human papil
31	2	28.6	8	12	O83332	O83332 murine hepa
32	2	28.6	9	2	Q51349	Q51349 pseudomonas
33	2	28.6	9	2	Q3E20	Q3ez0 streptococc
34	2	28.6	9	2	Q9R9C4	Q9rc4 borrelia bu
35	2	28.6	9	2	O8GL26	O8gl26 borrelia bu
36	2	28.6	9	4	O9BYF9	O9byf9 homo sapien
37	2	28.6	9	4	Q15891	Q15891 homo sapien
38	2	28.6	9	4	Q9H4B1	Q9h4b1 homo sapien
39	2	28.6	9	4	Q9UG54	Q9uge4 homo sapien
40	2	28.6	9	4	P78484	P78484 homo sapien
41	2	28.6	9	4	Q9UQW0	Q9uqw0 homo sapien
42	2	28.6	9	4	Q14277	Q14277 homo sapien
43	2	28.6	9	4	Q96P57	Q96p57 homo sapien
44	2	28.6	9	8	Q9MMF4	Q9mmf4 buteo rufin
45	2	28.6	9	8	Q9TKF2	Q9tkf2 asteromyrtu

ALIGNMENTS

RESULT 1
Q9N6M5
ID Q9N6M5 PRELIMINARY; PRT; 8 AA.
AC Q9N6M5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Dihydrofolate reductase thymidylate synthase (Fragment).
GN FOL1.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH, COUGAR TC751G34, SEA OTTER TC828G1, and BEVERLEY;
RA Lehmann T., Blackston C.R., Parmley S.F., Remington J.S., Dubey J.P.;
RT "Strain Typing of Toxoplasma gondii: Comparison of Antigen-Coding and Housekeeping Genes."
RL J. Parasitol. 0:0-0(2000).
DR EMBL; AF249695; AAF79153.1; -
DR EMBL; AF249692; AAF79150.1; -
DR EMBL; AF249693; AAF79151.1; -
DR EMBL; AF249694; AAF79152.1; -
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1035 MW; 33CAAAA05B133044 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IKE 3
|||
Db 2 IKE 4

RESULT 2
Q9NP06

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ID Q9NP06 PRELIMINARY; PRT; 10 AA.
AC Q9NP06;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator (Fragment).
GN CFTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92058253; PubMed=1719770;
RA Schwarz M., Summers C., Heptinstall L., Newton C., Markham A.,
RA Super M.;
RT "A deletion mutation of the cystic fibrosis transmembrane conductance
RT regulator (CFTR) locus: Delta I507.";
RL Adv. Exp. Med. Biol. 290:393-398(1991).
DR EMBL; S64643; AAB20219.2; -.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1107 MW; 58CFCC79C0544B13 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IKE 3
Db |||
2 IKE 4

RESULT 3
Q9NP07 PRELIMINARY; PRT; 10 AA.
ID Q9NP07;
AC Q9NP07;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator (Fragment).
GN CFTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92058253; PubMed=1719770;
RA Schwarz M., Summers C., Heptinstall L., Newton C., Markham A.,
RA Super M.;
RT "A deletion mutation of the cystic fibrosis transmembrane conductance
RT regulator (CFTR) locus: Delta I507.";
RL Adv. Exp. Med. Biol. 290:393-398(1991).
DR EMBL; S64640; AAB20220.2; -.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1073 MW; 58CFCC7050544B13 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IKE 3
Db |||
2 IKE 4

RESULT 4
P72081 PRELIMINARY; PRT; 7 AA.
ID P72081

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P72081;
AC 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 3'-methylcephem hydroxylase (Fragment).
GN CEFF.
OS Nocardia lactamdurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96009872; PubMed=7557411;
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
RA Liras P.;
RT "Characterization of the cmcH genes of Nocardia lactamdurans and
RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
RT O-carbamoyltransferase for cephamycin biosynthesis.";
RL Gene 162:21-27(1995).
DR EMBL; Z21682; CAA79797.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
Db |||
6 TS 7

RESULT 5
Q8GL12 PRELIMINARY; PRT; 7 AA.
ID Q8GL12;
AC Q8GL12;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pf-50 protein (Fragment).
GN Pf-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-9.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N40;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142100; AAN17911.1; -.
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 7 AA; 849 MW; 6337244330569ED0 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
Db |||
3 IK 4

RESULT 6
Q8GL04 PRELIMINARY; PRT; 7 AA.
ID Q8GL04;
AC Q8GL04;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

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DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-5.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RC STRAIN=93-0107;
RP SEQUENCE FROM N.A.
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
  RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DDAJ databases.
DR EMBL; AY142103; AANI7848.1; -.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 914 MW; 6337244330504310 CRC64;

  Query Match      28.6%; Score 2; DB 2; Length 7;
  Best Local Similarity 100.0%; Pred. No. 8.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
Db 3 IK 4

RESULT 7
Q8GL00
ID Q8GL00 PRELIMINARY; PRT; 7 AA.
AC Q8GL00;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-13.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RC STRAIN=CA15;
RP SEQUENCE FROM N.A.
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
  RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY142106; AANI7857.1; -.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

  Query Match      28.6%; Score 2; DB 2; Length 7;
  Best Local Similarity 100.0%; Pred. No. 8.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
Db 4 IK 5

RESULT 8
Q9S6D5
ID Q9S6D5 PRELIMINARY; PRT; 8 AA.
AC Q9S6D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Putative Is30 transposase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;

  Query Match      28.6%; Score 2; DB 2; Length 8;
  Best Local Similarity 100.0%; Pred. No. 8.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
Db 7 KE 8

RESULT 9
Q9R7T2
ID Q9R7T2 PRELIMINARY; PRT; 8 AA.
AC Q9R7T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 1.0 kDa protein (Fragment).
GN YQFG.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RC STRAIN=K12;
RP SEQUENCE FROM N.A.
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
  Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
  Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
  Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
  Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
  Yano M., Horiuchi T.;
RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
  RT to the 12.7-28.0 min Region on the Linkage Map.";
RL DNA Res. 3:137-155(1996).
DR EMBL; D90705; BAA35310.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

  Query Match      28.6%; Score 2; DB 2; Length 8;
  Best Local Similarity 100.0%; Pred. No. 8.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
Db 7 KE 8

RESULT 10
Q8RJI0
ID Q8RJI0 PRELIMINARY; PRT; 8 AA.
AC Q8RJI0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DNA replication initiation protein (Fragment).
OS DNAA-Like.
GN Streptomyces caespitosus.
OC Bacteria; Actinobacteria; Actinomycetales;
  Actinomycetaceae; Streptomyces.
OX NCBI_TaxID=562;

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OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=53502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC27422;
RA Ma W., Mao X., Jie L., Qin Z.J., Jiang W.H., Chiao R.S., Zhao G.P.;
RT "Cloning, sequence analysis and function analysis of the replication
RL origin oric of Streptovorticillum caespitosus ATCC27422.";
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ458440; CAD30324.1; -
FT NON_TER 1
SQ SEQUENCE 8 AA; 915 MW; 04744330440451A7 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
DB ||
5 IK 6

RESULT 11
P77556
ID P77556 PRELIMINARY; PRT; 8 AA.
AC P77556;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE TRAY (Fragment).
GN TRAY.
OS Escherichia coli.
OG Plasmid IncFII R1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOR11;
RX MEDLINE=96400908; PubMed=8807284;
RA Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;
RT "Mosaic structure of plasmids from natural populations of Escherichia
RT coli.";
RL Genetics 143:1091-1100(1996).
DR EMBL; U50661; AAC44245.1; -
DR EMBL; U50650; AAC44234.1; -
DR EMBL; U50651; AAC44235.1; -
DR EMBL; U50652; AAC44236.1; -
DR EMBL; U50653; AAC44237.1; -
DR EMBL; U50654; AAC44238.1; -
DR EMBL; U50655; AAC44239.1; -
DR EMBL; U50656; AAC44240.1; -
DR EMBL; U50657; AAC44241.1; -
DR EMBL; U50658; AAC44242.1; -
DR EMBL; U50659; AAC44243.1; -
DR EMBL; U50660; AAC44244.1; -
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 8 AA; 834 MW; D335A5B0544735A1 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB ||
1 TS 2

RESULT 12
Q56759
ID Q56759 PRELIMINARY; PRT; 8 AA.
AC Q56759;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Haloacid dehalogenase (Fragment).
GN DHALB.
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GJ10, and CV. M50;
RX MEDLINE=9517113; PubMed=7868610;
RA Van der Pijeg J., Willemssen M., van Hall G., Jaanssen D.B.;
RT "Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to
RT activation and mobilization of the haloacetate dehalogenase gene by
RT insertion element IS1247.";
RL J. Bacteriol. 177:1348-1356(1995).
DR EMBL; X84038; CAA58857.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
DB ||
2 IK 3

RESULT 13
Q9R9E0
ID Q9R9E0 PRELIMINARY; PRT; 8 AA.
AC Q9R9E0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Stage V sporulation protein E (Fragment).
GN SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=93003529; PubMed=1391053;
RA Henriques A.O., de Lencastre H., Piggot P.J.;
RT "A Bacillus subtilis morphogene cluster that includes spoVE is
RT homologous to the mra region of Escherichia coli.";
RL Biochimie 74:735-748(1992).
DR EMBL; X64258; CAA45556.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 893 MW; BE75A1A33321B1A6 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB ||
6 TS 7

RESULT 14
Q8G940
ID Q8G940 PRELIMINARY; PRT; 8 AA.
AC Q8G940;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.

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OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-9, and Plasmid group cp32-12.
OC Bacteria: Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DN127cl9-2, and Sh-2-82;
RC PLASMID-group cp32-9, and group cp32-12;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT phages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142104; AAN17853.1; -;
DR EMBL; AY142097; AAN17907.1; -;
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1042 MW; 1437244330504373 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IK 2
Db 4 IK 5

RESULT 15
P87225
ID P87225 PRELIMINARY; PRT; 8 AA.
AC P87225;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE GIN11 protein (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
CX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Scharfe M., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA WPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z73169; CAA97518.2; -;
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1019 MW; 4E21A9C449D5B73B CRC64;

Query Match 28.6%; Score 2; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FT 6
Db 6 FT 7

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Search completed: September 24, 2003, 16:45:21
 Job time : 69.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:32:04 : Search time 15.75 Seconds
(without alignments)
20.901 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7

Sequence: 1 IKEYFTS 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 369

Minimum DB seq length: 4

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	42.9	6	ASP2_LACSN	P82655 lactobacilli
2	2	28.6	5	RE31_LITRU	P82072 litoria rub
3	2	28.6	5	RE32_LITRU	P82073 litoria rub
4	2	28.6	7	FAR2_ASCSU	P31890 ascaris suu
5	2	28.6	7	WNA3_ACHFU	P35921 achatina fu
6	2	28.6	8	ACL_THUAL	P18691 thunnus alb
7	2	28.6	8	AKH_LIBAU	P25418 libellula a
8	2	28.6	8	AKH_TABAT	P14595 tabanus atr
9	2	28.6	8	HTF2_PERAM	P04549 periplaneta
10	2	28.6	8	LMT2_LOGMI	P22396 locusta mig
11	2	28.6	8	LPK_LEUMA	P13049 leucophaea
12	2	28.6	8	ORMY_ORCLI	P82455 orconectes
13	2	28.6	9	CCAP_CARMA	P38556 carcinus ma
14	2	28.6	9	COXE_THUOB	P80975 thunnus obe
15	2	28.6	9	KNL3_BOMVA	P83058 bombyna var
16	2	28.6	9	NEOU_CAVPO	P34966 cavia porce
17	2	28.6	9	NEUX_HUMAN	P04277 homo sapien
18	2	28.6	9	OXYF_SCYCA	P42997 scyllorhinu
19	2	28.6	9	OXYT_OCTUV	P80027 octopus vul
20	2	28.6	9	UHA2_HUMAN	P40929 homo sapien
21	2	28.6	9	YBFR_AZOVI	P25825 azotobacter
22	2	28.6	10	GON1_CHEPR	P80677 chelyosoma
23	2	28.6	10	HTF1_ROMMI	P18110 romalea mic
24	2	28.6	10	HTF2_CARMO	P11385 carausius m
25	2	28.6	10	HTF_TABAT	P14596 tabanus atr
26	2	28.6	10	LPK2_LOGMI	P41488 locusta mig
27	2	28.6	10	SVK_CAMUP	Q46464 campylobact
28	2	28.6	10	UZA6_HUMAN	P30090 homo sapien
29	2	28.6	10	UZA6_CHLTR	P38007 chlamydia t
30	1	14.3	4	ACHL_ACHFU	P35904 achatina fu
31	1	14.3	4	DCMS_PSECH	P19918 pseudomonas
32	1	14.3	4	EOSI_HUMAN	P02731 homo sapien
33	1	14.3	4	FAR3_HIRME	P42562 hirudo medi

34 1 14.3 4 1 FAR4_HIRME P42563 hirudo medi
35 1 14.3 4 1 FFXA_ANTEL P58705 anthopleura
36 1 14.3 4 1 FLRF_HIRME P42561 hirudo medi
37 1 14.3 4 1 FLRN_ANTEL P58707 anthopleura
38 1 14.3 4 1 FMRF_WACNI P01162 macrocallis
39 1 14.3 4 1 FYRI_ANTEL P58706 anthopleura
40 1 14.3 4 1 OCP1_OCTMI P58648 octopus min
41 1 14.3 4 1 OCP3_OCTMI P58649 octopus min
42 1 14.3 4 1 RM01_YEAST P36515 saccharomyc
43 1 14.3 4 1 TUFT_HUMAN P01858 homo sapien
44 1 14.3 5 1 ALI4_CARMA P81817 carcinus ma
45 1 14.3 5 1 BIOA_CITFR P13071 citrobacter

ALIGNMENTS

RESULT 1
ASP2_LACSN STANDARD; PRT; 6 AA.
ID ASP2_LACSN
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CBI;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CBI.";
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.
FT NON_TER 6
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEY 4
Db 2 KEY 4

RESULT 2
RE31_LITRU STANDARD; PRT; 5 AA.
ID RE31_LITRU
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic activity.


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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FT 6
Db 4 FT 5

RESULT 3
RE32_LITRU
ID RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
ON NCBI_TaxID=104895;
RX [1]
RP SEQUENCE.
RC TISSUE-Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FT 6
Db 4 FT 5

RESULT 4
FAR2_ASCSU
ID FAR2_ASCSU STANDARD; PRT; 7 AA.
AC P31890;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF2.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
ON NCBI_TaxID=6253, 6233;
RX [1]
RP SEQUENCE.
RC SPECIES=A.suum;
RX MDLINE=93324431; PubMed=8332542;
RA Cowden C., Stretton A.O.W.;
RT "AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
RL Peptides 14:423-430(1993).

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RN [2]
RP SEQUENCE.
RX SPECIES=P.redivivus;
RX MDLINE=95060998; PubMed=7970891;
RA Maule A.G., Shaw C., Bowman J.W.;
RT "The FMRamide-like neuropeptide AF2 (Ascaris suum) is present in the
RT free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida).";
RL Parasitology 109:351-356(1994).
CC -!- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.
CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
CC -!- SIMILARITY: BELONGS TO THE FAP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EY 4
Db 3 EY 4

RESULT 5
WWA3_ACHFU
ID WWA3_ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wwamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
ON NCBI_TaxID=6530;
RX [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR: S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KE 3
Db 2 KE 3

RESULT 6
ACI_THUAL
ID ACI_THUAL STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scombriformes; Scombroidei;
OC Scombridae; Thunnus.

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OS NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88376322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RL muscle.";
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
DB 4 IK 5

RESULT 7
AKH_LIBAU STANDARD; PRT; 8 AA.
AC P23418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: S10596; S10596.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FT 6
DB 4 FT 5

RESULT 8
AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE (DCC I).

OS NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88376322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RL muscle.";
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FT 6
DB 4 FT 5

RESULT 9
HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplaneta CC-2)
DE (Pea-CAH-II) (Led-CC-II) (Hypertrehalosaemic neuropeptide II).
OS Periplaneta americana (American cockroach), beetle), and
OS Lepidoptera decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]

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RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
RL beetle and the American cockroach are identical.";
RN Peptides 10:1287-1289(1989).
[4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RN the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Graptodorrhina portentosus, Blattella germanica and Blattella orientalis
RN and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
DR Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FT 6
DB 4 FT 5
RESULT 10
LMT2_LOCMI STANDARD; PRT; 8 AA.
AC P22396;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamytotropin 2 (LOM-MT-2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamytotropin II, an
RT additional neuropeptide of Locusta migratoria. Member of the
RT cephalomyotropic peptide family.";
RL Insect Biochem. 20:479-484(1990).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
DR Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;
Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FT 6
DB 4 FT 5

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FT 6
DB 4 FT 5
RESULT 11
LPK_LEUMA STANDARD; PRT; 8 AA.
AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leukopyrokinin (LPK) (LEM-PK).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86269041; PubMed=3015140;
RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RN Leucopyrokinin: structure-function studies.";
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
RN [2]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of a blocked myotropic
RN neuropeptide isolated from the cockroach, Leucophaea maderae.";
RL Comp. Biochem. Physiol. 85C:219-224(1986).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
CC PENTAPEPTIDE FRAGMENT FTPLR.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A23967; A23967.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
DR Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 TS 7
DB 2 TS 3
RESULT 12
ORMY_ORCLI STANDARD; PRT; 8 AA.
AC P82455;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orcomytotropin (OMT).
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidae; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;

RN [1]
 RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
 RC TISSUE=Hindgut;
 RX MEDLINE=20411310; PubMed=10952880;
 RA Dirksen H., Burdick S., Sauter A., Keller R.;
 RT "Two orckins and the novel octapeptide orcomyotropin in the hindgut
 of the crayfish *Orconectes limosus*: identified myostimulatory
 RT neuropeptides originating together in neurones of the terminal
 abdominal ganglion.";
 RL J. Exp. Biol. 203:2807-2818(2000).
 CC -!- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
 CC BY ABDOMINAL GANGLIONIC NEURONS.
 CC -!- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
 KW Amidation; Neuropeptide.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FT 6
 DB 4 FT 5

RESULT 13
 CCAP_CARMA
 ID CCAP_CARMA STANDARD; PRT; 9 AA.
 AC P38556;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cardioactive peptide (CCAP).
 OS Carcinus maenas (Common shore crab) (Green crab),
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
 OS Tenebrio molitor (Yellow mealworm), and
 OS Spodoptera eridania (Southern armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC XNBL_TaxID=6759, 7130, 7067, 37547;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.maenas; TISSUE=Pericardial organs;
 RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
 RT shore crab *Carcinus maenas*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=M.sexta;
 RX MEDLINE=93050243; PubMed=1426284;
 RA Cheung C.-C., Ioi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
 RT "Primary structure of a cardioactive neuropeptide from the tobacco
 RT hawkmoth, *Manduca sexta*.";
 RL FEBS Lett. 313:165-168(1992).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
 RX MEDLINE=94176032; PubMed=6129851;
 RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
 RA Schooley D.A.;
 RT "Isolation and identification of a cardioactive peptide from *Tenebrio
 RT molitor* and *Spodoptera eridania*.";
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
 CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
 CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
 CC INTO THE HEMOLYMPH.
 DR PIR; A26363; A26363.
 DR PIR; S27233; S27233.
 KW Neuropeptide; Amidation.

FT DISULFID 3 9
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;
 Amidation.
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FT 6
 DB 6 FT 7

RESULT 14
 COXE_THUOB
 ID COXE_THUOB STANDARD; PRT; 9 AA.
 AC P80975;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
 OS Thunus obesus (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OC NCBL_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocchrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
 DR PIR; S77984; S77984.
 DR InterPro: IPR001349; COX6A.
 DR PROSITE; PS01329; COX6A; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KE 3
 DB 1 KE 2

RESULT 15
 KNL3_BOMVA
 ID KNL3_BOMVA STANDARD; PRT; 9 AA.
 AC P83058;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE [Thr6]bradykinin.
 OS Bombina variegata (Yellow-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OC NCBL_TaxID=8348;
 RN [1]

RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FT 6
||
Db 5 FT 6

Search completed: September 24, 2003, 16:43:16
Job time : 16.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:39:35 ; Search time 28.5833 Seconds
(without alignments)
23.552 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7

Sequence: 1 IKEYPTS 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1077

Minimum DB seq length: 4

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3	42.9	9	2	A24244	adipokinetic hormo
2	3	42.9	10	2	D61440	polygalacturonase
3	2	28.6	5	2	B37325	pap fibrinolyt regul
4	2	28.6	5	2	P70278	Ig heavy chain CRD
5	2	28.6	5	2	P70644	T-cell receptor be
6	2	28.6	5	2	H44817	34.5K structural p
7	2	28.6	5	2	F44817	34.5K structural p
8	2	28.6	5	2	B44817	34.5K structural p
9	2	28.6	5	2	D44817	35K structural pro
10	2	28.6	6	2	S02617	alcohol dehydrogen
11	2	28.6	6	2	A31263	dihydrofolate redu
12	2	28.6	7	2	S17976	glucose isomerase
13	2	28.6	7	2	P50254	18K protein 5507 -
14	2	28.6	7	2	S33244	neuromodulatory pe
15	2	28.6	7	2	PC1316	large granule L3 c
16	2	28.6	7	2	A38671	peptidylglycine mo
17	2	28.6	7	2	A38081	amine oxidase (cop
18	2	28.6	7	4	A58725	virotaxin - destro
19	2	28.6	8	2	A32523	peptidyl-di-peptida
20	2	28.6	8	2	S08996	hypertrehalosemic
21	2	28.6	8	2	S10596	adipokinetic hormo
22	2	28.6	8	2	B49823	adipokinetic hormo
23	2	28.6	8	2	B44960	neuropeptide led-c
24	2	28.6	8	2	A33995	adipokinetic hormo
25	2	28.6	8	2	S53310	adipokinetic hormo
26	2	28.6	8	2	A58620	adipokinetic hormo
27	2	28.6	8	2	S20162	leghemoglobin III
28	2	28.6	8	2	A31570	angiotensin-conver
29	2	28.6	8	2	S16324	hypothetical prote

30	2	28.6	8	2	A21440	variant surface gl
31	2	28.6	8	2	A23967	leucopyrokinin - M
32	2	28.6	8	2	B27867	homeotic protein U
33	2	28.6	8	2	S71919	alcohol dehydrogen
34	2	28.6	8	2	B45800	serum albumin - do
35	2	28.6	8	2	A42057	fibroblast growth
36	2	28.6	8	2	A61597	cytochrome P450 AL
37	2	28.6	8	2	S65296	Na+-transporting A
38	2	28.6	8	2	A59028	MHC class I histoc
39	2	28.6	9	2	A61357	phyllotaerulein -
40	2	28.6	9	2	D58503	translation elonga
41	2	28.6	9	2	JQ1202	leader peptide - p
42	2	28.6	9	2	A61358	bradykinin-like pe
43	2	28.6	9	2	A61057	Thr-6 bradykinin -
44	2	28.6	9	2	A26744	bradykinin-like pe
45	2	28.6	9	2	A60579	bradykinin-like pe

ALIGNMENTS

RESULT 1

A24244

adipokinetic hormone - bollworm

N:Alternate names: Hez-AKH

C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)

C>Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997

C:Accession: A24244

R:Jaife, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Rldg Biochem. Biophys. Res. Commun. 135, 622-628, 1986

A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of He

A:Reference number: A24244; MUID:86186794; PMID:3964263

A:Accession: A24244

A:Molecule type: protein

A:Residues: 1-9 <JAF>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7

Db 4 FTS 6

RESULT 2

D61440

polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)

C:Species: Aspergillus sp.

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 06-Dec-1996

C:Accession: D61440

R:Stratilova, E.; Markovic, O.; Skrovina, D.; Rexova-Benkova, L.; Jornvall, H.

J. Protein Chem. 12, 15-22, 1993

A:Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and s

A:Reference number: A61440; MUID:93151962; PMID:8427629

A:Accession: D61440

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <STR>

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 42.9%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7

Db 5 FTS 7

```

RESULT 3
B37325
pap fibrial regulatory protein papI - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993
C;Accession: B37325
R;Braaten, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.
J. Bacteriol. 173, 1789-1800, 1991
A;Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus ex
A;Reference number: A37325; MUID:911514136; PMID:1671857
A;Accession: B37325
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <BRA>
A;Cross-references: GB:M63747

Query Match 28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EV 4
||
Db 3 EV 4

RESULT 4
PT0278
Iq heavy chain CRD3 region (clone 4-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0278
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0278
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YF 5
||
Db 1 YF 2

RESULT 5
PT0644
T-cell receptor beta chain V-D-J region (111-LG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0644
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0644
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FT 6
||

```

```

Db 4 FT 5

RESULT 6
B44817
34.5K structural protein - Leuconostoc oenos phage P32 (fragment)
C;Species: Leuconostoc oenos phage P32
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: B44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: B44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBI:70332)

Query Match 28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
||
Db 3 TS 4

RESULT 7
F44817
34.5K structural protein - Leuconostoc oenos phage P54 (fragment)
C;Species: Leuconostoc oenos phage P54
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: F44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: F44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBI:70335)

Query Match 28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
||
Db 3 TS 4

RESULT 8
B44817
34.5K structural protein - Leuconostoc oenos phage P211-15 (fragment)
C;Species: Leuconostoc oenos phage P211-15
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: B44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: B44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBI:70342)

Query Match 28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
||

```

```

Db          3 TS 4

RESULT 9
D44817
35k structural protein - Leuconostoc oenos phage PAT5-12 (fragment)
C:Species: Leuconostoc oenos phage PAT5-12
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: D44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: D44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBIP:70340)

Query Match      28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TS 7
      ||
Db      3 TS 4

RESULT 10
S02617
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-1997
C:Accession: S02617
R:Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joernvall
FEBS Lett. 222, 99-103, 1987
A:Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differences
A:Reference number: S02617; MUID:88005160; PMID:3653405
A:Accession: S02617
A:Molecule type: protein
A:Residues: 1-6 <FA>
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match      28.6%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IK 2
      ||
Db      5 IK 6

RESULT 11
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886; PMID:2904149
A:Accession: A31263
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match      28.6%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TS 7

Db          3 TS 4

RESULT 12
S17976
glucose isomerase - Thermoanaerobacterium saccharolyticum (fragment)
C:Species: Thermoanaerobacterium saccharolyticum
C:Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 17-Apr-1998
C:Accession: S17976
R:Lee, C.; Zeikus, J.G.
Biochem. J. 273, 565-571, 1991
A:Title: Purification and characterization of thermostable glucose isomerase from Clo
A:Reference number: S15119; MUID:91144536; PMID:1396956
A:Accession: S17976
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <LEE>
A:Note: the sequence from page 568 is inconsistent with that from page 565 in having
A:Note: the source is designated as Thermoanaerobacter strain B6A

Query Match      28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YF 5
      ||
Db      4 YF 5

RESULT 13
PS0254
18k protein 5507 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C:Accession: PS0254
R:Tsuigita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0254
A:Molecule type: protein
A:Residues: 1-7 <TSU>
A:Experimental source: leaf, chloroplast, strain Nihonbare
A:Note: molecular weight 18k, pI 4.4

Query Match      28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KE 3
      ||
Db      5 KE 6

RESULT 14
S33244
neuromodulatory peptide Wamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia c
A:Reference number: S33244; MUID:93265912; PMID:8495720
A:Accession: S33244
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match      28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY 2 KE 3
||
Db 2 KE 3

RESULT 15

PC1316
large granule L3 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
C;Species: Tachyplesus tridentatus
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: PC1316
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
J.; Biochem. 114, 307-316, 1993
A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridenta
A;Reference number: PC1309; MUID:94110249; PMID:8282718
A;Accession: PC1316
A;Molecule type: protein
A;Residues: 1-7 <SH1>
C;Comment: This protein participates in immobilization of invading microbes.

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
||
Db 1 TS 2

Search completed: September 24, 2003, 16:46:16
Job time : 28.5833 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:45:30 ; Search time 46.0833 Seconds
(without alignments)
22.983 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7

Sequence: 1 IKEYFTS 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 566894 seqs, 151307093 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75270

Minimum DB seq length: 4

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	4	57.1	7	12	US-10-197-927-5
2	4	57.1	9	11	US-09-277-074-34
3	4	57.1	9	12	US-10-006-177-17
4	4	57.1	9	15	US-10-006-869-2791
5	4	57.1	10	7	US-08-344-824-70
6	4	57.1	10	8	US-08-452-843A-20
7	4	57.1	10	11	US-09-572-404B-2153
8	4	57.1	10	11	US-09-802-083-7
9	4	57.1	10	12	US-10-172-785-7
10	4	57.1	10	15	US-10-006-869-2792
11	4	57.1	10	15	US-10-165-732A-7
12	3	42.9	4	12	US-09-800-187-35
13	3	42.9	4	12	US-09-800-187-36
14	3	42.9	4	15	US-10-206-699-23
15	3	42.9	5	10	US-09-859-214-42

16	3	42.9	5	11	US-09-911-129B-13	Sequence 13, Appl
17	3	42.9	5	14	US-10-006-630-2	Sequence 2, Appl
18	3	42.9	5	14	US-10-020-436A-5	Sequence 5, Appl
19	3	42.9	5	14	US-10-020-436A-14	Sequence 14, Appl
20	3	42.9	5	15	US-10-105-735-54	Sequence 54, Appl
21	3	42.9	5	15	US-10-206-699-163	Sequence 163, Appl
22	3	42.9	6	9	US-09-895-072-31	Sequence 31, Appl
23	3	42.9	6	9	US-09-876-388-6	Sequence 6, Appl
24	3	42.9	6	9	US-09-839-447A-52	Sequence 52, Appl
25	3	42.9	6	10	US-09-986-552-31	Sequence 31, Appl
26	3	42.9	6	10	US-09-727-963A-25	Sequence 25, Appl
27	3	42.9	6	12	US-10-306-686-31	Sequence 31, Appl
28	3	42.9	6	15	US-10-153-271-52	Sequence 52, Appl
29	3	42.9	6	15	US-10-287-892-6	Sequence 6, Appl
30	3	42.9	6	15	US-10-288-340-6	Sequence 6, Appl
31	3	42.9	7	9	US-09-056-160B-5	Sequence 5, Appl
32	3	42.9	7	9	US-09-056-160B-124	Sequence 124, App
33	3	42.9	7	9	US-09-876-388-7	Sequence 7, Appl
34	3	42.9	7	9	US-09-839-447A-51	Sequence 51, Appl
35	3	42.9	7	9	US-09-898-461-2	Sequence 2, Appl
36	3	42.9	7	9	US-09-898-461-17	Sequence 17, Appl
37	3	42.9	7	9	US-09-898-461-18	Sequence 18, Appl
38	3	42.9	7	9	US-09-898-461-19	Sequence 19, Appl
39	3	42.9	7	9	US-09-898-461-20	Sequence 20, Appl
40	3	42.9	7	11	US-09-954-385-423	Sequence 423, App
41	3	42.9	7	12	US-10-190-082-155	Sequence 155, App
42	3	42.9	7	12	US-10-190-082-421	Sequence 421, App
43	3	42.9	7	12	US-10-286-457-149	Sequence 149, App
44	3	42.9	7	12	US-10-119-528-28	Sequence 28, Appl
45	3	42.9	7	15	US-10-043-487-439	Sequence 439, App

ALIGNMENTS

RESULT 1
US-10-197-927-5
; Sequence 5, Application US/10197927
; Publication No. US20030166138A1
; GENERAL INFORMATION:
; APPLICANT: Kinellia, Todd
; APPLICANT: Onashi, Cara
; APPLICANT: Anderson, Dave
; TITLE OF INVENTION: Cyclic Peptides and Analogs Useful to Treat Allergies
; FILE REFERENCE: RIGL-002/0105
; CURRENT APPLICATION NUMBER: US/10/197,927
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/358,827
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically synthesized cyclic peptide
US-10-197-927-5

Query Match 57.1%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YFTS 7
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Db 2 YFTS 5

RESULT 2
US-09-277-074-34
; Sequence 34, Application US/09277074
; Publication No. US20030022820A1
; GENERAL INFORMATION:

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; APPLICANT: Sherman, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR2155S
; CURRENT APPLICATION NUMBER: US/09/277,074
; CURRENT FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-277-074-34

Query Match      57.1%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 EYFT 6
Db      5 EYFT 8

RESULT 3
US-10-006-177-17
; Sequence 17, Application US/10006177
; Publication No. US2003016513A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishna, Venky
; APPLICANT: Philip, Ramila
; TITLE OF INVENTION: Cytotoxic T-Lymphocyte-Inducing Immunogens for Prevention, Treatm
; TITLE OF INVENTION: Diagnosis of Cancer
; FILE REFERENCE: 26747-35
; CURRENT APPLICATION NUMBER: US/10/006,177
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US/60/251,022
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US/60/256,824
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitopic Peptide
US-10-006-177-17

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IKEY 4
Db      6 IKEY 9

RESULT 4
US-10-006-869-2791
; Sequence 2791, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
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; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2791
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-10-006-869-2791

Query Match      57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 EYFT 6
Db      1 EYFT 4

RESULT 5
US-08-344-824-70
; Sequence 70, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-344-824-70

Query Match      57.1%; Score 4; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IKEY 4
Db      1 IKEY 4
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Db          7 IKEY 10

RESULT 6
US-08-452-843A-20
; Sequence 20, Application US/08452843A
; Publication No. US20020098197A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 399632001321
; CURRENT APPLICATION NUMBER: US/08/452.843A
; CURRENT FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53, 321-330
US-08-452-843A-20

Query Match          57.1%; Score 4; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 EYFT 6
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Db          6 EYFT 9

RESULT 7
US-09-572-404B-2153
; Sequence 2153, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2153
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C6 at 364-373 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-572-404B-2153

Query Match          57.1%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 YFTS 7
           ||||
Db          2 YFTS 5

RESULT 8
US-09-802-083-7
; Sequence 7, Application US/09802083
; Publication No. US20030119075A1
; GENERAL INFORMATION:
; APPLICANT: Kirchhofer, Daniel K.

Db          7 IKEY 10
; APPLICANT: Lowe, David G.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-Tissue Factor Antibodies with Enhanced
; TITLE OF INVENTION: Anticoagulant Potency
; FILE REFERENCE: P1736R1
; CURRENT APPLICATION NUMBER: US/09/802.083
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-083-7

Query Match          57.1%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 IKEY 4
           ||||
Db          4 IKEY 7

RESULT 9
US-10-172-785-7
; Sequence 7, Application US/10172785
; Publication No. US20030143225A1
; GENERAL INFORMATION:
; APPLICANT: Refino, Canio J.
; APPLICANT: Bunting, Stuart
; APPLICANT: Kirchhofer, Daniel
; TITLE OF INVENTION: COMBINATIONS OF ANTI-TISSUE FACTOR ANTIBODIES AND ANTICOAGULANT
; TITLE OF INVENTION: ANTIPLATELET AGENTS
; FILE REFERENCE: 11669.1100SI2
; CURRENT APPLICATION NUMBER: US/10/172.785
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/165,732
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 09/802,083
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-172-785-7

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 IKEY 4
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Db          4 IKEY 7

RESULT 10
US-10-006-869-2792
; Sequence 2792, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006.869
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; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2792
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-10-006-869-2792

Query Match          57.1%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EYF 6
Db 1 EYF 4

RESULT 11
US-10-165-732A-7
; Sequence 7, Application US/10165732A
; Publication No. US20030124117A1
; GENERAL INFORMATION:
; APPLICANT: Refino, Canio J.
; APPLICANT: Bunting, Stuart
; APPLICANT: Kirchhofer, Daniel
; TITLE OF INVENTION: COMBINATIONS OF ANTI-TISSUE FACTOR ANTIBODIES AND ANTICOAGULANT A
; TITLE OF INVENTION: ANTIPLATELET AGENTS
; FILE REFERENCE: 11669.110US11
; CURRENT APPLICATION NUMBER: US/10/165.732A
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/802,083
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-165-732A-7

Query Match          57.1%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IKEY 4
Db 4 IKEY 7

RESULT 12
US-09-800-187-35
; Sequence 35, Application US/09800187
; Publication No. US20030129724A1
; GENERAL INFORMATION:
; APPLICANT: GROZINGER, CHRISTINA M.
; APPLICANT: HASSIG, CHRISTIAN A.
; APPLICANT: SCHREIBER, STUART L.
; TITLE OF INVENTION: CLASS II HUMAN HISTONE DEACETYLASES, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: HUV-037.01
; CURRENT APPLICATION NUMBER: US/09/800,187
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,802
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35

; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2792
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-187-35

Query Match          42.9%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EYF 5
Db 1 EYF 3

RESULT 13
US-09-800-187-36
; Sequence 36, Application US/09800187
; Publication No. US20030129724A1
; GENERAL INFORMATION:
; APPLICANT: GROZINGER, CHRISTINA M.
; APPLICANT: HASSIG, CHRISTIAN A.
; APPLICANT: SCHREIBER, STUART L.
; TITLE OF INVENTION: CLASS II HUMAN HISTONE DEACETYLASES, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: HUV-037.01
; CURRENT APPLICATION NUMBER: US/09/800,187
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,802
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-187-36

Query Match          42.9%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EYF 5
Db 1 EYF 3

RESULT 14
US-10-206-699-23
; Sequence 23, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-23
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Query Match 42.9%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
Db 1 FTS 3

Db 2 FTS 4

Search completed: September 24, 2003, 16:58:28
Job time : 46.0833 secs

RESULT 15
US-09-859-214-42
; Sequence 42, Application US/09859214
; Patent No. US20020103111A1
; GENERAL INFORMATION:
; APPLICANT: Schwender, Charles F.
; Shroff, Hitesh N.
; TITLE OF INVENTION: INHIBITORS OF MACAM-1-MEDIATED
; INTERACTIONS AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,214
; FILING DATE: 16-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/109,879
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/582,740
; FILING DATE: 04-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-12A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= modified aa
; /note= "Ac - Leucine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= modified aa
; /note= "Leucine - NH2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-859-214-42

Query Match 42.9%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
Db 1 FTS 3

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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:40:45 ; Search time 23.3333 Seconds
(without alignments)
12.693 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7

Sequence: 1 IKEYTTS 7

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Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 89050

Minimum DB seq length: 4

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Post-processing: Listing first 45 summaries

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4: /cgn2.6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2.6/ptodata/1/iaa/PCRUS.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	4	57.1	10	4	US-09-187-859-2792
5	4	57.1	10	4	US-09-839-542B-2792
6	3	42.9	4	1	US-08-416-007-3
7	3	42.9	4	2	US-08-475-751-3
8	3	42.9	5	1	US-08-244-646-3
9	3	42.9	5	1	US-08-737-757-3
10	3	42.9	5	2	US-08-574-959A-11
11	3	42.9	5	2	US-08-432-016-7
12	3	42.9	5	2	US-08-684-594-7
13	3	42.9	5	3	US-08-582-740-42
14	3	42.9	5	3	US-08-469-141A-20
15	3	42.9	5	3	US-08-469-141A-71
16	3	42.9	5	3	US-08-591-632-24
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18	3	42.9	5	3	US-09-357-014-11
19	3	42.9	5	4	US-09-267-993-2
20	3	42.9	5	4	US-09-611-451-24
21	3	42.9	5	4	US-09-306-542A-54
22	3	42.9	5	5	PCT-US95-13794-20
23	3	42.9	5	5	PCT-US95-13794-71
24	3	42.9	6	1	US-08-237-731-4
25	3	42.9	6	1	US-08-290-448A-41
26	3	42.9	6	1	US-08-290-448A-41
27	3	42.9	6	1	US-08-175-069A-41

28 3 42.9 6 2 US-08-528-523-4 Sequence 4, Appli
29 3 42.9 6 3 US-08-893-654B-16 Sequence 16, Appl
30 3 42.9 6 3 US-09-243-374-28 Sequence 28, Appl
31 3 42.9 6 4 US-09-623-618B-6 Sequence 6, Appl
32 3 42.9 6 4 US-08-461-939B-41 Sequence 41, Appl
33 3 42.9 6 4 US-08-464-000-41 Sequence 41, Appl
34 3 42.9 6 4 US-09-556-600-52 Sequence 52, Appl
35 3 42.9 6 4 US-09-657-332A-6 Sequence 6, Appl
36 3 42.9 6 4 US-09-635-872A-31 Sequence 31, Appl
37 3 42.9 6 4 US-09-636-077A-31 Sequence 31, Appl
38 3 42.9 6 5 PCT-US95-10793-4 Patent No. 5188642
39 3 42.9 6 6 5188642-7 Patent No. 5188642
40 3 42.9 6 6 5310667-19 Patent No. 5310667
41 3 42.9 7 1 US-08-137-614A-31 Sequence 31, Appl
42 3 42.9 7 1 US-08-297-731-5 Sequence 5, Appl
43 3 42.9 7 1 US-07-942-245-500 Sequence 500, App
44 3 42.9 7 2 US-08-317-310A-18 Sequence 18, Appl
45 3 42.9 7 4 US-09-623-618B-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-187-859-2791
; Sequence 2791, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187.859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2791
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2791

Query Match 57.1%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6

Db 1 EYFT 4

RESULT 2

US-09-839-542B-2791
; Sequence 2791, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839.542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2791
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-839-542B-2791

Query Match
Best Local Similarity 57.1%; Score 4; DB 4; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
Db 1 EYFT 4
|||||

RESULT 3
PCT-US95-16415-34
; Sequence 34, Application PC/TUS9516415
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
; TITLE OF INVENTION: CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16415
; FILING DATE: 13-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,558
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: 433.1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-16415-34

Query Match
Best Local Similarity 57.1%; Score 4; DB 5; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
Db 5 EYFT 8
|||||

RESULT 4
US-09-187-859-2792
; Sequence 2792, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
```

```
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187.859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2792.
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2792

Query Match
Best Local Similarity 57.1%; Score 4; DB 4; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
Db 1 EYFT 4
|||||

RESULT 5
US-09-839-542B-2792
; Sequence 2792, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839.542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2792
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-839-542B-2792

Query Match
Best Local Similarity 57.1%; Score 4; DB 4; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
Db 1 EYFT 4
|||||

RESULT 6
US-08-416-007-3
; Sequence 3, Application US/08416007
; Patent No. 5693679
; GENERAL INFORMATION:
; APPLICANT: Vincent, Jean-Pierre
; APPLICANT: Gaudriault, Georges
; APPLICANT: Beaudet, Alain
; TITLE OF INVENTION: FLUORESCENT SOMATOSTATIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
```


; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,007
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06942/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-416-007-3

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
Db 1 FTS 3

RESULT 7
US-08-475-751-3
; Sequence 3, Application US/08475751
; Patent No. 5824772
; GENERAL INFORMATION:
; APPLICANT: Vincent, Jean-Pierre
; APPLICANT: Gaudriault, Georges
; APPLICANT: Beaudet, Alain
; TITLE OF INVENTION: FLUORESCENT SOMATOSTATIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 585 Commercial Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-1024
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,751
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,007
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06942/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/723-4123
; TELEFAX: 617/723-8962

; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-475-751-3

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
Db 1 FTS 3

RESULT 8
US-08-244-646-3
; Sequence 3, Application US/08244646
; Patent No. 574692
; GENERAL INFORMATION:
; APPLICANT: Cervone, Felice
; APPLICANT: De Lorenzo, Giulia
; APPLICANT: Salvi, Giovanni
; APPLICANT: Albersheim, Peter
; APPLICANT: Darvill, Alan
; APPLICANT: Bergmann, Carl
; TITLE OF INVENTION: Nucleotide Sequences Coding An
; TITLE OF INVENTION: Endopolygalacturonase Inhibitor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sally A. Sullivan
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,646
; FILING DATE: 06-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT RM 91A 000915
; FILING DATE: 06-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IT/00158
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sullivan, Sally A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 19-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Phaseolus vulgaris

;
; STRAIN: Pinto
; US-08-244-646-3

Query Match 42.9%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FTS 7
|||
Db 2 FTS 4

RESULT 9
US-08-737-757-3
; Sequence 3, Application US/08737757
; Patent No. 5783413
; GENERAL INFORMATION:
; APPLICANT: Pedersen, John
; APPLICANT: Lauritzen, Conni
; APPLICANT: Madsen, Mads Thorup
; TITLE OF INVENTION: An enzymatic process for
; TITLE OF INVENTION: producing a desired protein from an amino terminally extended
; TITLE OF INVENTION: protein
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, PC
; STREET: 805 Third Avenue - 27th Floor
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,757
; FILING DATE: 05-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Agda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/0C596
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-757-3

Query Match 42.9%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FTS 7
|||
Db 3 FTS 5

RESULT 10
US-08-574-959A-11
; Sequence 11, Application US/08574959A
; Patent No. 596224

;
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-574-959A-11

Query Match 42.9%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IKE 3
|||
Db 3 IKE 5

RESULT 11
US-08-432-016-7
; Sequence 7, Application US/08432016
; Patent No. 5968788
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: PATEL, DHAVALKUMAR
; APPLICANT: BOWEN, MICHAEL A.
; APPLICANT: MARQUARDT, HANS
; TITLE OF INVENTION: CD6 LIGAND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,016
; FILING DATE: 01-MAY-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-432-016-7

Query Match 42.9%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IKE 3
Db 1 IKE 3

RESULT 12
US-08-684-594-7
Sequence 7, Application US/08684594
Patent No. 5998172
GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: PATEL, DHAVALKUMAR
APPLICANT: BOWEN, MICHAEL A.
APPLICANT: MARQUARDT, HANS
TITLE OF INVENTION: CD6 LIGAND
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,594
FILING DATE: 18-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,016
FILING DATE: 01-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-112

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-684-594-7

Query Match 42.9%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IKE 3
Db 1 IKE 3

RESULT 13
US-08-582-740-42
Sequence 42, Application US/08582740
Patent No. 6037324
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: Inhibitors of MacCAM-1-Mediated
TITLE OF INVENTION: Interactions and Methods of Use Therefor
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,740
FILING DATE: 04-JAN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= modified aa
OTHER INFORMATION: /note= "Ac - Leucine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= modified aa
OTHER INFORMATION: /note= "Leucine - NH2"
US-08-582-740-42

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
|||
Db 2 FTS 4

RESULT 14
US-08-469-141A-20
; Sequence 20, Application US/08469141A
; Patent No. 6124107
; GENERAL INFORMATION:
; APPLICANT: MUMFORD, RICHARD A.
; APPLICANT: DAVIES, D.T. PHILIP
; APPLICANT: DAHLGREN, MARY E.
; APPLICANT: BOGER, JOSHUA S.
; APPLICANT: HUMES, JOHN L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DR. CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,141A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 174611B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)-594-6734
; TELEFAX: (908)-594-4720
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-469-141A-20

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
|||
Db 1 FTS 3

RESULT 15
US-08-469-141A-71
; Sequence 71, Application US/08469141A
; Patent No. 6124107
; GENERAL INFORMATION:
; APPLICANT: MUMFORD, RICHARD A.
; APPLICANT: DAVIES, D.T. PHILIP

; APPLICANT: DAHLGREN, MARY E.
; APPLICANT: BOGER, JOSHUA S.
; APPLICANT: HUMES, JOHN L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DR. CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,141A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 174611B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)-594-6734
; TELEFAX: (908)-594-4720
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-469-141A-71

Query Match 42.9%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
|||
Db 1 FTS 3

Search completed: September 24, 2003, 16:47:04
Job time : 24.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 16:31:29 ; Search time 68.25 Seconds
(without alignments)
16.280 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7

Sequence: 1 IKEYRTS 7

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Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 250473

Minimum DB seq length: 4

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Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7	100.0	7	20 AAY49696	HIV-1 gp120 induce
2	4	57.1	5	22 AAB55781	PDZ motif sequence
3	4	57.1	5	22 AAB57613	Glycophorin C C-te
4	4	57.1	5	22 AAB58023	Glycophorin C C-te
5	4	57.1	5	23 ABJ05279	T-cell surface rec
6	4	57.1	5	23 ABP63507	PDZ motif (PL) pep
7	4	57.1	6	22 AAB55782	PDZ motif sequence
8	4	57.1	6	22 AAB57614	Glycophorin C C-te
9	4	57.1	6	22 AAB58024	Glycophorin C C-te

10	4	57.1	6	23 ABJ05280	T-cell surface rec
11	4	57.1	6	23 ABP63508	PDZ motif (PL) pep
12	4	57.1	7	22 AAB55783	PDZ motif sequence
13	4	57.1	7	22 AAB57613	Glycophorin C C-te
14	4	57.1	7	22 AAB58025	Glycophorin C C-te
15	4	57.1	7	23 ABJ05281	T-cell surface rec
16	4	57.1	7	23 ABP63509	PDZ motif (PL) pep
17	4	57.1	8	22 AAB55784	PDZ motif sequence
18	4	57.1	8	22 AAB57616	Glycophorin C C-te
19	4	57.1	8	22 AAB58026	Glycophorin C C-te
20	4	57.1	8	23 ABJ05282	T-cell surface rec
21	4	57.1	8	23 ABP63510	PDZ motif (PL) pep
22	4	57.1	9	15 AAR59225	Peptide fragment (
23	4	57.1	9	17 AAR97542	Antigenic peptide,
24	4	57.1	9	20 AAY53365	p53 epitope (aa 32
25	4	57.1	9	20 AAY40188	Amino acid sequenc
26	4	57.1	9	20 AAY26704	HLA-A2 binding p53
27	4	57.1	9	21 AAY63307	Protocadherin.cel
28	4	57.1	9	22 AAG89489	p53 DR 3a motif bi
29	4	57.1	9	22 AAB76335	Pf CSP immunogenic
30	4	57.1	9	23 ABG32317	HLA-A1/A2 associat
31	4	57.1	9	23 ABJ01319	158PID7 related HL
32	4	57.1	9	23 ABJ01336	158PID7 related HL
33	4	57.1	9	24 ABP74569	Human SCP-1 epitop
34	4	57.1	10	17 AAR89381	p53 derived immuno
35	4	57.1	10	21 AAY63308	Protocadherin.cel
36	4	57.1	10	22 AAE12047	Humanised anti-tis
37	4	57.1	10	22 AAG59599	Human complementar
38	4	57.1	10	23 ABJ01365	158PID7 related HL
39	4	57.1	10	23 ABJ01398	158PID7 related HL
40	4	57.1	10	23 ABJ01702	158PID7 related HL
41	4	57.1	10	23 ABJ01731	158PID7 related HL
42	4	57.1	10	23 ABJ01829	158PID7 related HL
43	4	57.1	10	23 ABJ01938	158PID7 related HL
44	4	57.1	10	23 ABJ01942	158PID7 related HL
45	4	57.1	10	24 ABP74570	Human SCP-1 epitop

ALIGNMENTS

RESULT 1
AAY49696
ID AAY49696 standard; peptide; 7 AA.
AC AAY49696;
DT 18-JAN-2000 (first entry)
XX HIV-1 gp120 induced neuronal cell death inhibiting peptide #2.
DE XX Neurological degenerative disease; HIV-1; envelope protein; gp120;
KW toxic; neuron; accessory glial cell; chemokine; viral infection;
KW neuronal cell death; encephalopathy; neuropathy; memory loss;
KW dementia; depression; psychosis; opportunistic infection;
KW neurotoxicity; inflammatory neurological disease; multiple sclerosis;
KW tropical spastic paraparesis; Alzheimer's disease.
XX Synthetic.
OS XX
PN W09951254-A1.
XX
PD 14-OCT-1999.
XX
PF 06-APR-1999; 99WO-US07514.
XX
PR 06-APR-1998; 98US-0080836.
XX
PA (ADIM-) ADVANCED IMMUNIT INC.
XX
PI Pert C, Ruff M;
XX
DR WPI; 1999-633695/54.

XX New peptides useful for inhibiting human immuno-deficiency virus type 1
 PT (HIV-1) gp120 induced neuronal cell death -
 XX Claim 1; Page 11; 16pp; English.
 PS
 CC AAY49695 and AAY49696 represent peptides which inhibit HIV-1 gp120
 CC induced neuronal cell death. Pharmaceutical compositions containing the
 CC peptides are useful for treating symptoms caused by neuronal cell loss.
 CC Such conditions especially associated with HIV infection include
 CC encephalopathies, neuropathies, memory loss, dementia, depression,
 CC psychosis and opportunistic infections. The peptides act as antagonists
 CC of gp120-mediated neurotoxicity and subsequent neuronal degeneration.
 CC This enables therapeutic treatment of HIV infection and other
 CC inflammatory neurological diseases, including multiple sclerosis,
 CC tropical spastic paraparesis and Alzheimer's disease.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IKEYFTS 7
 DB 1 IKEYFTS 7
 RESULT 2
 AAB55781
 ID AAB55781 standard; Peptide; 5 AA.
 AC AAB55781;
 XX
 XX 07-MAR-2001 (first entry)
 DT
 XX PDZ motif sequence #12.
 DE
 XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
 KW allergy; asthma; multiple sclerosis; cancer; infection.
 KW
 XX Synthetic.
 OS
 XX WO200069896-A2.
 PN
 XX 23-NOV-2000.
 PD
 XX 12-MAY-2000; 2000WO-US13161.
 PF
 XX 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0182296.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 XX Lu PS;
 PI
 XX WPI; 2001-080245/09.
 DR
 XX Modulating a biological function of an endothelial cell or
 XX hematopoietic cell, useful for treating autoimmune diseases and
 PT infectious diseases, by administering an antagonist that inhibits
 PT binding between a PDZ protein and a PL protein -
 XX
 PS Disclosure; Page 87-94; 141pp; English.
 XX

CC The present invention relates to a new method for modulating a
 CC biological function of an endothelial cell or hematopoietic cell. The
 CC method involves introducing into a cell, an antagonist that inhibits
 CC binding between a PDZ protein and a PL protein. The inhibitor is used
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
 CC disease. It may also be used to prevent transplantation rejection of
 CC a solid organ transplant. The method may also be used in the treatment
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.
 XX
 SQ Sequence 5 AA;
 Query Match 57.1%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEYF 5
 DB 1 KEYF 4
 RESULT 3
 AAB57613
 ID AAB57613 standard; Peptide; 5 AA.
 XX
 AC AAB57613;
 XX
 XX 12-MAR-2001 (first entry)
 DT
 XX Glycophorin C C-terminal core sequence #2.
 DE
 XX Endothelial cell; hematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.
 XX
 XX Homo sapiens.
 OS
 XX WO200069897-A2.
 PN
 XX 23-NOV-2000.
 PD
 XX 12-MAY-2000; 2000WO-US13166.
 PF
 XX 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 XX Lu PS;
 PI
 XX WPI; 2001-025003/03.
 DR
 XX New inhibitors of binding of a PDZ protein and PL protein for
 PT inhibiting T cell-mediated response by hematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses, e.g. inflammation, cancer -
 XX

PS Disclosure; Page 93; 139pp; English.
 XX
 CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and zonula occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX
 SQ Sequence 5 AA;
 Query Match 57.1%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEYF 5
 Db ||||
 1 KEYF 4
 RESULT 4
 AAB58023
 ID AAB58023 standard; Peptide; 5 AA.
 XX
 AC AAB58023;
 XX
 DT 12-MAR-2001 (first entry)
 XX
 DE Glycophorin C C-terminal core sequence #2.
 XX
 KW Endothelial cell; hematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200069898-A2.
 XX
 XX 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WO-US13205.
 XX
 PR 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX
 XX (ARBO-) ARBOR VITA CORP.
 PA Rabinowitz JD, Lu PS, Schweizer J;
 XX WPI; 2002-416878/44.

PI Lu PS;
 XX
 DR WPI; 2001-061214/07.
 XX
 PT Modulating a biological function of a hematopoietic cell for treating
 PT an allergic response, or diseases mediated by immune system cells,
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or
 PT inhibitor -
 XX
 XX Disclosure; Page 95; 143pp; English.
 XX
 CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and zonula occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX
 SQ Sequence 5 AA;
 Query Match 57.1%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEYF 5
 Db ||||
 1 KEYF 4
 RESULT 5
 ABJ05279
 ID ABJ05279 standard; Peptide; 5 AA.
 XX
 AC ABJ05279;
 XX
 DT 07-NOV-2002 (first entry)
 XX
 DE T-cell surface receptor C-terminal core peptide SEQ ID No 274.
 XX
 KW Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
 KW inflammatory; humoral immune response; inflammation; C-terminal core;
 KW T-cell surface receptor.
 XX
 OS Unidentified.
 XX
 PN WO200231512-A2.
 XX
 PD 18-APR-2002.
 XX
 XX 11-OCT-2001; 2001WO-US32150.
 PF
 XX 13-OCT-2000; 2000US-0688017.
 PR
 XX (ARBO-) ARBOR VITA CORP.
 PA Rabinowitz JD, Lu PS, Schweizer J;
 XX WPI; 2002-416878/44.

XX Assays for determining the affinity of binding between a PDZ domain and
PT a ligand, and determining the KI of an inhibitor of the binding, PDZ
PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ
PT domain -
XX
XX Disclosure; Page 117; 164pp; English.

XX The invention relates to methods and reagents for determining the
CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The
CC invention also relates to methods and reagents for determining the KI of
CC an inhibitor of binding between a PDZ domain and a ligand, identifying an
CC agent that enhances binding of a PDZ domain and a ligand, and determining
CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by
CC determining the ligand bound with an immobilised polypeptide comprising a
CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,
CC an inhibitor) of interaction between PDZ and PL is useful for treating a
CC disease characterised by leukocyte activation, e.g., an autoimmune
CC disease that is characterised by inflammatory or humoral immune response,
CC and for reducing inflammation in a subject. This sequence represents a T-
CC cell surface receptor C-terminal core peptide relating to the PDZ
CC containing proteins of the invention.

XX Sequence 5 AA;
SQ

Query Match 57.1%; Score 4; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 KEYF 5
Db 1 KEYF 4

RESULT 6
ABP63507
XX ABP63507 standard; Peptide; 5 AA.
XX
XX ABP63507;
XX
XX 28-OCT-2002 (first entry)
XX
XX PDZ motif (PL) peptide SEQ ID NO:234.
XX
XX Molecular interaction; haematopoietic cell; immune response; T cell;
KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;
KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;
KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;
KW antiulcer; antipsoriatic; dermatological; antiasthmatic; cytotstatic;
KW antimicrobial; vasotropic; inflammatory immune response; inflammation;
KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;
KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;
KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;
KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;
KW angiogenesis-dependent disorder; infectious disease.

XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200242422-A2.
XX
XX 30-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US44138.
XX
XX 11-NOV-2000; 2000US-0710059.
XX 24-NOV-2000; 2000US-0721915.
XX 24-NOV-2000; 2000US-0722069.
XX 28-NOV-2000; 2000US-0724553.
XX (ARBO-) ARBOR VITA CORP.
XX
XX Lu P, Rabinowitz JD, Schweizer J;

XX WPI; 2002-608221/65.
XX
XX Modulating the biological function of an endothelial cell or
PT hemotopoietic cell e.g., a T-cell or B-cell comprises introducing into
PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ
PT ligand protein in the cell -
XX
XX Disclosure; Page 135; 207pp; English.

XX The present invention describes a method (M1) for modulating a biological
CC function of an endothelial cell or haematopoietic cell. M1 comprises
CC introducing into the cell, an agent that inhibits binding of a PDZ
CC (PSD95, Drosophila large protein, and Zonula Occludin 1 protein)
CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the
CC biological function. Also described is a method (M2) for determining
CC whether a test compound is an inhibitor of binding between a PDZ protein
CC and a PL protein. M1 is used for modulating a biological function of an
CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an
CC inflammatory or humoral immune response, or an autoimmune disease. An
CC inhibitor (I) is useful for treating a disease characterised by leukocyte
CC activation, where the disease is characterised by an inflammatory or
CC humoral immune response, e.g., an autoimmune disease. The compounds
CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating
CC symptoms of) a variety of diseases and conditions characterised by
CC inflammatory and humoral immune responses e.g., inflammation, allergy,
CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,
CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic
CC diseases such as asthma, allergic rhinitis, transplantation rejection
CC (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,
CC autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,
CC angiogenesis-dependent disorders, infectious diseases and ischaemia.
CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 5 AA;
SQ

Query Match 57.1%; Score 4; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 KEYF 5
Db 1 KEYF 4

RESULT 7
AAB55782
XX AAB55782 standard; Peptide; 6 AA.
XX
XX AAB55782;
XX
XX 07-MAR-2001 (first entry)
XX
XX PDZ motif sequence #13.
XX
XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
KW allergy; asthma; multiple sclerosis; cancer; infection.
XX
XX Synthetic.
XX
XX WO200069896-A2.
XX
XX 23-NOV-2000.
XX
XX 12-MAY-2000; 2000WO-US13161.
XX
XX 14-MAY-1999; 99US-0134114.
XX 14-MAY-1999; 99US-0134117.
XX 14-MAY-1999; 99US-0134118.
XX 21-OCT-1999; 99US-0160860.
XX 29-OCT-1999; 99US-0162498.
XX 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 PI Lu PS;
 XX
 DR WPI; 2001-080245/09.
 XX
 XX Modulating a biological function of an endothelial cell or
 PT hematopoietic cell, useful for treating autoimmune diseases and
 PT infectious diseases, by administering an antagonist that inhibits
 PT binding between a PDZ protein and a PL protein -
 XX
 PS Disclosure; Page 87-94; 141pp; English.
 XX
 CC The present invention relates to a new method for modulating a
 CC biological function of an endothelial cell or hematopoietic cell. The
 CC method involves introducing into a cell, an antagonist that inhibits
 CC binding between a PDZ protein and a PL protein. The inhibitor is used
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
 CC disease. It may also be used to prevent transplantation rejection of
 CC a solid organ transplant. The method may also be used in the treatment
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.
 XX
 SQ Sequence 6 AA;
 Query Match 57.1%; Score 4; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KEYF 5
 Db 2 KEYF 5
 RESULT 8
 AAB57614
 ID AAB57614 standard; Peptide; 6 AA.
 XX
 AC AAB57614;
 XX
 DT 12-MAR-2001 (first entry)
 DE
 DE Glycophorin C C-terminal core sequence #3.
 XX
 KW Endothelial cell; haematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 PN W0200069897-A2.
 XX
 XX 23-NOV-2000.
 PD
 PF 12-MAY-2000; 2000WO-US13166.
 XX
 XX 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 PI Lu PS;
 XX
 DR WPI; 2001-025003/03.
 XX
 XX New inhibitors of binding of a PDZ protein and PL protein for
 PT inhibiting T cell-mediated response by hematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses, e.g. inflammation, cancer -
 XX
 PS Disclosure; Page 93; 139pp; English.
 XX
 CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and zonula Occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX
 SQ Sequence 6 AA;
 Query Match 57.1%; Score 4; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KEYF 5
 Db 2 KEYF 5
 RESULT 9
 AAB58024
 ID AAB58024 standard; Peptide; 6 AA.
 XX
 AC AAB58024;
 XX
 DT 12-MAR-2001 (first entry)
 DE
 DE Glycophorin C C-terminal core sequence #3.
 XX
 KW Endothelial cell; haematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 PN W0200069898-A2.

XX 23-NOV-2000.
 XX PD
 XX KW
 XX PF
 XX XX
 XX 12-MAY-2000; 2000WO-US13205.
 XX PR
 XX 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX PA
 XX (ARBO-) ARBOR VITA CORP.
 XX PI
 XX Lu PS;
 XX DR
 XX WPI; 2001-061214/07.
 XX PT
 XX Modulating a biological function of a hematopoietic cell for treating
 PT an allergic response, or diseases mediated by immune system cells,
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or
 PT inhibitor -
 XX PT
 XX PS
 XX Disclosure; Page 96; 143pp; English.
 XX CC
 XX The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of a
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and zonula occludens 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX CC
 XX SQ Sequence 6 AA;
 Query Match 57.1%; Score 4; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KEYF 5
 Db
 RESULT 10
 ABJ05280
 ID ABJ05280 standard; Peptide; 6 AA.
 XX AC
 XX ABJ05280;
 XX XX
 XX 07-NOV-2002 (first entry)
 XX T-cell surface receptor C-terminal core peptide SEQ ID NO 275.
 DE
 XX Immunosuppressive; antiinflammatory; affinity; Rd; binding; PDZ domain;
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
 KW

KW inflammatory; humoral immune response; inflammation; C-terminal core;
 KW T-cell surface receptor.
 XX
 XX OS
 XX Unidentified.
 XX WO200231512-A2.
 XX PN
 XX 18-APR-2002.
 XX PD
 XX 11-OCT-2001; 2001WO-US32150.
 PF
 XX 13-OCT-2000; 2000US-0688017.
 XX PR
 XX (ARBO-) ARBOR VITA CORP.
 XX PA
 XX Rabinowitz JD, Lu PS, Schweizer J;
 XX WPI; 2002-416878/44.
 XX DR
 XX Assays for determining the affinity of binding between a PDZ domain and
 PT a ligand, and determining the Ki of an inhibitor of the binding.
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ
 PT domain -
 XX PT
 XX Disclosure; Page 117; 164pp; English.
 XX PS
 XX The invention relates to methods and reagents for determining the
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The
 CC invention also relates to methods and reagents for determining the Ki of
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an
 CC agent that enhances binding of a PDZ domain and a ligand, and determining
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by
 CC determining the ligand bound with an immobilised polypeptide comprising a
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a
 CC disease characterised by leukocyte activation, e.g., an autoimmune
 CC disease that is characterised by inflammatory or humoral immune response,
 CC and for reducing inflammation in a subject. This sequence represents a T-
 CC cell surface receptor C-terminal core peptide relating to the PDZ
 CC containing proteins of the invention.
 XX CC
 XX SQ Sequence 6 AA;
 Query Match 57.1%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KEYF 5
 Db
 RESULT 11
 ABP63508
 ID ABP63508 standard; Peptide; 6 AA.
 XX AC
 XX ABP63508;
 XX XX
 XX 28-OCT-2002 (first entry)
 XX PDZ motif (PL) peptide SEQ ID NO:235.
 DE
 XX
 XX Molecular interaction; hematopoietic cell; immune response; T cell;
 KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;
 KW Drosophila large disc protein; zonula occludens 1 protein; PL protein;
 KW immunosuppressive; antiinflammatory; anti-allergic; antiatherosclerotic;
 KW antiulcer; antipsoriatic; dermatological; antiasthmatic; cytostatic;
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;
 KW angiogenesis-dependent disorder; infectious disease.

XX Homo sapiens.
OS Synthetic.
XX WO200242422-A2.
XX 30-MAY-2002.
XX 09-NOV-2001; 2001WO-US44138.
XX 11-NOV-2000; 2000US-0710059.
PR 24-NOV-2000; 2000US-0721915.
PR 24-NOV-2000; 2000US-0722069.
PR 28-NOV-2000; 2000US-0724553.
XX (ARBO-) ARBOR VITA CORP.
XX Lu P, Rabinowitz JD, Schweizer J;
XX WPI; 2002-608221/65.
XX Modulating the biological function of an endothelial cell or
PT hematopoietic cell e.g., a T-cell or B-cell comprises introducing into
PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ
PT ligand protein in the cell -
XX Disclosure; Page 135; 207pp; English.
XX The present invention describes a method (M1) for modulating a biological
CC function of an endothelial cell or hematopoietic cell. M1 comprises
CC introducing into the cell, an agent that inhibits binding of a PDZ
CC (PSD95, Drosophila large disc protein, and zonula Occludin 1 protein)
CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the
CC biological function. Also described is a method (M2) for determining
CC whether a test compound is an inhibitor of binding between a PDZ protein
CC and a PL protein. M1 is used for modulating a biological function of an
CC endothelial cell or hematopoietic cell e.g., T-cell or B-cell, by an
CC inflammatory or humoral immune response, or an autoimmune disease. An
CC inhibitor (I) is useful for treating a disease characterised by leukocyte
CC activation, where the disease is characterised by an inflammatory or
CC humoral immune response, e.g., an autoimmune disease. The compounds
CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating
CC symptoms of) a variety of diseases and conditions characterised by
CC inflammatory and humoral immune responses e.g., inflammation, allergy,
CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,
CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic
CC diseases such as asthma, allergic rhinitis, transplantation rejection
CC (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,
CC autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,
CC angiogenesis-dependent disorders, infectious diseases and ischaemia.
CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 6 AA;
Query Match 57.1%; Score 4; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEYF 5
Db ||||
2 KEYF 5
RESULT 12
AAB55783
ID AAB55783 standard; Peptide; 7 AA.
XX
AC AAB55783;
XX
XX 07-MAR-2001 (first entry)
DT
DE PDZ motif sequence #14.

XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
KW allergy; asthma; multiple sclerosis; cancer; infection.
XX Synthetic.
XX WO200069896-A2.
XX 23-NOV-2000.
XX 12-MAY-2000; 2000WO-US13161.
XX 14-MAY-1999; 99US-0134114.
PR 14-MAY-1999; 99US-0134117.
PR 14-MAY-1999; 99US-0134118.
PR 21-OCT-1999; 99US-0160860.
PR 29-OCT-1999; 99US-0162498.
PR 13-DEC-1999; 99US-0170453.
PR 14-JAN-2000; 2000US-0176195.
PR 14-FEB-2000; 2000US-0182296.
PR 11-APR-2000; 2000US-0196460.
PR 11-APR-2000; 2000US-0196527.
XX (ARBO-) ARBOR VITA CORP.
XX Lu PS;
XX WPI; 2001-080245/09.
XX Modulating a biological function of an endothelial cell or
PT hematopoietic cell, useful for treating autoimmune diseases and
PT infectious diseases, by administering an antagonist that inhibits
PT binding between a PDZ protein and a PL protein -
XX Disclosure; Page 87-94; 141pp; English.
XX The present invention relates to a new method for modulating a
CC biological function of an endothelial cell or hematopoietic cell. The
CC method involves introducing into a cell, an antagonist that inhibits
CC binding between a PDZ protein and a PL protein. The inhibitor is used
CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
CC disease. It may also be used to prevent transplantation rejection of
CC a solid organ transplant. The method may also be used in the treatment
CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
CC graft rejection, transplantation rejection), atherosclerosis, cancers,
CC infectious diseases, ischemia, vasculitis and Crohn's disease.
XX
SQ Sequence 7 AA;
Query Match 57.1%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEYF 5
Db ||||
3 KEYF 6
RESULT 13
AAB57615
ID AAB57615 standard; Peptide; 7 AA.
XX
AC AAB57615;
XX
XX 12-MAR-2001 (first entry)
DT
DE Glycophorin C C-terminal core sequence #4.
XX
XX Endothelial cell; hematopoietic cell; PDZ domain protein;
KW PL domain protein; leukocyte activation; T cell surface receptor;
XX

QY 2 KEYF 5
 Db 3 KEYF 6

RESULT 15

ABJ05281
 ID ABJ05281 standard; Peptide; 7 AA.
 XX
 AC ABJ05281;
 XX
 DT 07-NOV-2002 (first entry)
 XX
 DE T-cell surface receptor C-terminal core peptide SEQ ID No 276.
 XX
 KW immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
 KW inflammatory; humoral immune response; inflammation; C-terminal core;
 KW T-cell surface receptor.

XX Unidentified.

XX WO200231512-A2.

XX 18-APR-2002.

XX 11-OCT-2001; 2001WO-US32150.

XX 13-OCT-2000; 2000US-0688017.

XX (ARBO-) ARBOR VITA CORP.

XX Rabinowitz JD, Lu PS, Schweizer J;

XX WPI; 2002-416878/44.

XX Assays for determining the affinity of binding between a PDZ domain and
 PT a ligand, and determining the Ki of an inhibitor of the binding, PDZ
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ
 PT domain -

XX Disclosure; Page 117; 164pp; English.

XX The invention relates to methods and reagents for determining the
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The
 CC invention also relates to methods and reagents for determining the Ki of
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an
 CC agent that enhances binding of a PDZ domain and a ligand, and determining
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by
 CC determining the ligand bound with an immobilised polypeptide comprising a
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a
 CC disease characterised by leukocyte activation, e.g., an autoimmune
 CC disease that is characterised by inflammatory or humoral immune response,
 CC and for reducing inflammation in a subject. This sequence represents a T-
 CC cell surface receptor C-terminal core peptide relating to the PDZ
 CC containing proteins of the invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEYF 5
 Db 3 KEYF 6

Search completed: September 24, 2003, 16:42:42
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